



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 188362

TO: Brendan O Baggot
Location: rem/2B59/2C18
Art Unit: 1638
Friday, May 05, 2006

Case Serial Number: 10/620914

From: Deirdre Arnold
Location: Biotech-Chem Library
REM 1A55
Phone: 571-272-2532

Deirdre.Arnold@uspto.gov

Search Notes

RUSH

Please feel free to contact me if you have any questions or would like to amend the search.

Thank you for using STIC services.

Regards,
Deirdre Arnold

REMOVE
PENDING



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GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: May 4, 2006, 18:51:48 ; Search time 1620 Seconds
(without alignments)
9938.567 Million cell updates/sec

Title: US-10-620-914-44

Perfect score: 1947
Sequence: 1 atggggctggctgacgg.....gcgcgaagaagacaactaa 1947

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134699005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA Main:*

- 1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq.*
- 2: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq.*
- 3: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq.*
- 4: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq.*
- 5: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq.*
- 6: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq.*
- 7: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq.*
- 8: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq.*
- 9: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq.*
- 10: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1947	100.0	1947	7	US-10-620-914-44
2	645	33.1	5242	7	US-10-620-914-43
3	100.2	5.1	1252	5	US-10-118-495-1
4	100.2	5.1	1252	7	US-10-620-914-1
5	76.8	3.9	2259	8	US-10-741-849-6021
6	73	3.7	2727	7	US-10-620-914-49
7	73	3.7	3427	7	US-10-620-914-48
8	72.4	3.7	137560	8	US-10-481-112-1
9	70	3.6	1251	5	US-10-118-495-32
10	70	3.6	1251	7	US-10-620-914-32
11	69.6	3.6	1248	5	US-10-118-495-22
12	69.6	3.6	1248	7	US-10-620-914-22
13	67.8	3.5	1104	6	US-10-204-434A-12
14	67.8	3.5	6798	3	US-09-918-740-57
15	67.8	3.5	6798	6	US-10-204-434A-13
16	67.8	3.5	6798	8	US-10-835-516-57
17	67.8	3.5	6798	10	US-11-053-541-57
18	67.8	3.5	8077	3	US-09-918-740-63
19	67.8	3.5	8077	10	US-10-835-516-63
20	67.8	3.5	8077	10	US-11-053-541-63
21	67.6	3.5	5858	8	US-10-488-056-14
22	66.6	3.4	1626	7	US-10-392-041-3
23	66.6	3.4	1626	7	US-10-394-763-3

24	66.6	3.4	1626	8	US-10-392-387-3	Sequence 3, Appli
25	65	3.3	1530	6	US-10-402-842-12	Sequence 12, Appl
26	65	3.3	1530	7	US-10-746-795-12	Sequence 12, Appl
27	65	3.3	11238	5	US-10-205-032-15	Sequence 15, Appl
28	65	3.3	47988	6	US-10-402-842-1	Sequence 1, Appli
29	65	3.3	48200	7	US-10-746-795-1	Sequence 1, Appli
30	65	3.3	60196	5	US-10-205-032-1	Sequence 1, Appli
31	64.6	3.3	2034	7	US-10-441-949-56	Sequence 56, Appl
32	64.6	3.3	2289	7	US-10-437-963-62879	Sequence 62879, A
33	64.2	3.3	2278	9	US-10-812-271-7	Sequence 7, Appli
34	64.2	3.3	2737	8	US-10-425-115-146880	Sequence 146880, A
35	64.2	3.3	2807	7	US-10-425-114-33804	Sequence 33804, A
36	64.2	3.3	2807	8	US-10-425-115-146911	Sequence 146911, A
37	63.4	3.3	2550	3	US-09-967-464-65	Sequence 65, Appl
38	63.2	3.2	1737	8	US-10-411-910A-230	Sequence 230, App
39	63	3.2	2034	7	US-10-441-949-57	Sequence 57, Appl
40	62.6	3.2	1251	5	US-10-118-495-28	Sequence 28, Appl
41	62.6	3.2	1251	7	US-10-620-914-28	Sequence 28, Appl
42	62.6	3.2	1276	7	US-10-425-114-30664	Sequence 30664, A
43	62.4	3.2	982	8	US-10-727-010-1	Sequence 1, Appli
44	62.4	3.2	1082	3	US-09-881-165-4	Sequence 4, Appli
45	62.2	3.2	1350	8	US-10-411-910A-271	Sequence 271, App

ALIGNMENTS

RESULT 1
US-10-620-914-44
; Sequence 44, Application US/10620914
; Publication No. US20040093639A1
; GENERAL INFORMATION:
; APPLICANT: Benning, Christoph
; APPLICANT: Riekhof, Wayne
; APPLICANT: Klug, Rouven
; TITLE OF INVENTION: Compositions and Methods for the Production of Betaine Lipids
; FILE REFERENCE: MSU-07769
; CURRENT APPLICATION NUMBER: US/10/620,914
; CURRENT FILING DATE: 2003-07-16
; PRIOR APPLICATION NUMBER: 10/118,495
; PRIOR FILING DATE: 2002-04-08
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 44
; LENGTH: 1947
; TYPE: DNA
; ORGANISM: Chlamydomonas reinhardtii
US-10-620-914-44

Query Match		100.0%	Score 1947;	DB 7;	Length 1947;
Best Local Similarity		100.0%	Pred. No. 0;		
Matches 1947;		Conservative	0;	Mismatches	0; Gaps 0;
Qy	1	ATGGGGTGGGTCGTGACGGCGCGCGCTCGDAGCTACACCAAGAGAACTTCTCCCTGGAG	60		
Db	1	ATGGGGTGGGTCGTGACGGCGCGCGCTCGDAGCTACACCAAGAGAACTTCTCCCTGGAG	60		
Qy	61	AAGCTCAAGCTCAGCAGCATGAAGATGACTGACCGCTTCTGCGCCATATGGTTCCGC	120		
Db	61	AAGCTCAAGCTCAGCAGCATGAAGATGACTGACCGCTTCTGCGCCATATGGTTCCGC	120		
Qy	121	AGCAAGAGGGCGATGATCAGCTGCTGCGCTGGAGAGCTTCTACGGGCCCCAGGCCGCT	180		
Db	121	AGCAAGAGGGCGATGATCAGCTGCTGCGCTGGAGAGCTTCTACGGGCCCCAGGCCGCT	180		
Qy	181	GCCTTTCCTGCGCGCGCGCGCGCTCGDAGCTACCTCATCTGGTTCGCTGGTTCGC	240		
Db	181	GCCTTTCCTGCGCGCGCGCGCGCTCGDAGCTACCTCATCTGGTTCGCTGGTTCGC	240		
Qy	241	ACTGGGAGAGATGTCGATATGATGGCTGATTACATCGACCTGGCGAAGTTCAGTCCATC	300		
Db	241	ACTGGGAGAGATGTCGATATGATGGCTGATTACATCGACCTGGCGAAGTTCAGTCCATC	300		

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QY 301 TACGTGTCGACCTGTGTGCACTCGTGTGCGAGTGGCCAAAGAAAGGCGAAAGGCCCAAG 360
Db |||
QY 301 TACGTGTCGACCTGTGTGCACTCGTGTGCGAGTGGCCAAAGAAAGGCGAAAGGCCCAAG 360
Db |||
QY 361 GGCTGGAAGAAATGTCAGGTCGTGTGAGGCGCAGCGTGTGCCAAATTTGGCCGCCCTTGAGGGC 420
Db |||
QY 361 GGCTGGAAGAAATGTCAGGTCGTGTGAGGCGCAGCGTGTGCCAAATTTGGCCGCCCTTGAGGGC 420
Db |||
QY 421 ACCGGAGCGTCATACACCTTCTCTACTCGCTCAGATGATTCACCGTTCCACAAAGTC 480
Db |||
QY 421 ACCGGAGCGTCATACACCTTCTCTACTCGCTCAGATGATTCACCGTTCCACAAAGTC 480
Db |||
QY 481 ATCGACAGGCTGTGCTGTACTGTCGCAAGAGCGCTGTGGGCTGTGCGACTTCTAC 540
Db |||
QY 481 ATCGACAGGCTGTGCTGTACTGTCGCAAGAGCGCTGTGGGCTGTGCGACTTCTAC 540
Db |||
QY 541 GTGAGCGGCAAGTAGACCTTGCCTCCCTGCGCCAGATGCCCTCGCGCGTTCTTCTG 600
Db |||
QY 541 GTGAGCGGCAAGTAGACCTTGCCTCCCTGCGCCAGATGCCCTCGCGCGTTCTTCTG 600
Db |||
QY 601 CGATCGATCTTCGACATCGACAAATTCGATCGGCTCGGAGCGCGCGCTTACCTGGAG 660
Db |||
QY 601 CGATCGATCTTCGACATCGACAAATTCGATCGGCTCGGAGCGCGCGCTTACCTGGAG 660
Db |||
QY 661 CAGAACTGGAGCGCGTGTGGAGCAGAAACACCAAGGTTTCGATCCCTACGTGCGGTG 720
Db |||
QY 661 CAGAACTGGAGCGCGTGTGGAGCAGAAACACCAAGGTTTCGATCCCTACGTGCGGTG 720
Db |||
QY 721 CTGCGCGCCCTACTACTAGTGTGATGTCGCGCCCTGCCCCAGTGTGGCCACGCCCTGCAC 780
Db |||
QY 721 CTGCGCGCCCTACTACTAGTGTGATGTCGCGCCCTGCCCCAGTGTGGCCACGCCCTGCAC 780
Db |||
QY 781 GAGAGCGCGTGGAGCGCGCCGCTGATGAGATCAACCCAAAGGACACGCGTGTGAC 840
Db |||
QY 781 GAGAGCGCGTGGAGCGCGCCGCTGATGAGATCAACCCAAAGGACACGCGTGTGAC 840
Db |||
QY 841 GAGACCCCGAGCGGATATGAGGTGATGAGATCAACCCAAAGGACACGCGTGTGAC 900
Db |||
QY 841 GAGACCCCGAGCGGATATGAGGTGATGAGATCAACCCAAAGGACACGCGTGTGAC 900
Db |||
QY 901 CTGACTAGCGCGGTGCAATGCCCTGAACTGTGTGTCAGGGGCGCGCGAGTGTG 960
Db |||
QY 901 CTGACTAGCGCGGTGCAATGCCCTGAACTGTGTGTCAGGGGCGCGCGAGTGTG 960
Db |||
QY 961 TCGGTGATCTCAACCCCGCGAGTCGCGCTTCTGGAGCTGAAAGAGTGGCCATTGAG 1020
Db |||
QY 961 TCGGTGATCTCAACCCCGCGAGTCGCGCTTCTGGAGCTGAAAGAGTGGCCATTGAG 1020
Db |||
QY 1021 CAGCTGAGATTTGAGGAGCTGTGGCAGCTGTCGCGAGGCGTGCACCCGCGCATTTGAG 1080
Db |||
QY 1021 CAGCTGAGATTTGAGGAGCTGTGGCAGCTGTCGCGAGGCGTGCACCCGCGCATTTGAG 1080
Db |||
QY 1081 GAGCTGTACGAGAAGAGTGGCGCCCTTCTGTGCGAAACACGACCACTTCTGTGTC 1140
Db |||
QY 1081 GAGCTGTACGAGAAGAGTGGCGCCCTTCTGTGCGAAACACGACCACTTCTGTGTC 1140
Db |||
QY 1141 AAGCGCTCTGGTACTTCCAGACGGCTGTACTACGAGGCGGATGGGCAAGCTGTC 1200
Db |||
QY 1141 AAGCGCTCTGGTACTTCCAGACGGCTGTACTACGAGGCGGATGGGCAAGCTGTC 1200
Db |||
QY 1201 TGGGTGTCGAGTGTGCTGGCGTGTGTCGGAATGGGCAAGACCGTCAAGCGCTGCGC 1260
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QY 1201 TGGGTGTCGAGTGTGCTGGCGTGTGTCGGAATGGGCAAGACCGTCAAGCGCTGCGC 1260
Db |||
QY 1261 AACCGGCCCAATGGAGGAGCAGCGCGTGTGTGGGACAGCAATGCTCATCACTTC 1320
Db |||
QY 1261 AACCGGCCCAATGGAGGAGCAGCGCGTGTGTGGGACAGCAATGCTCATCACTTC 1320
Db |||
QY 1321 GTGAGAACGGGCGCCAGCGCTGTGTGCTGTGTCGATGAGTGTGAGCGCTGGTCTC 1380
Db |||
QY 1321 GTGAGAACGGGCGCCAGCGCTGTGTGCTGTGTCGATGAGTGTGAGCGCTGGTCTC 1380
Db |||
QY 1381 TTCAACAAGGCGTGTGTGTTGCGGCGCGCGTGTGCGGGCAAGCAGTACGCGCTGATC 1440
Db |||
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Db 1381 TTCAACAAGGCGTGTGTGTTGCGGCGCGCTGCGGGCAAGCAGTACGCGCTGATC 1440
QY 1441 AAGCGGAGCGGATCCCATTTGAGAACTAATATCGCGGCAACATGAGCGGTCGCGGAG 1500
Db 1441 AAGCGGAGCGGATCCCATTTGAGAACTAATATCGCGGCAACATGAGCGGTCGCGGAG 1500
QY 1501 AACTCGCAACTGCGGCAAGCAGAACTTCTTACTTACTTACTTACTTACTTACTTACTTACTT 1560
Db 1501 AACTCGCAACTGCGGCAAGCAGAACTTCTTACTTACTTACTTACTTACTTACTTACTTACTT 1560
QY 1561 CGCGACAATGCGCCCACTTCTGCGGAGCGGCTTTCGCCACCTTCAAGAGTGGCGTG 1620
Db 1561 CGCGACAATGCGCCCACTTCTGCGGAGCGGCTTTCGCCACCTTCAAGAGTGGCGTG 1620
QY 1621 GTGACAACTGACCGTCTCCACCACTTCTTCAATGAGAGCTCAAGCGCGCACCTAC 1680
Db 1621 GTGACAACTGACCGTCTCCACCACTTCTTCAATGAGAGCTCAAGCGCGCACCTAC 1680
QY 1681 ACCAAGTGTATCTGATGGACCACTGTCGCTGGATATGCCGTGGCCAAAGCTG 1740
Db 1681 ACCAAGTGTATCTGATGGACCACTGTCGCTGGATATGCCGTGGCCAAAGCTG 1740
QY 1741 GCCAGTGCCTGGCCAAAGCAGTTCGCGCGGCGGCTTCGTCATCTGGCGCTCCGCTCC 1800
Db 1741 GCCAGTGCCTGGCCAAAGCAGTTCGCGCGGCGGCTTCGTCATCTGGCGCTCCGCTCC 1800
QY 1801 CTCAGCGCGCTTACGCGGAGCTGATCCAGAAAGCGGCTTCGAGCTGCGCTGATCCGC 1860
Db 1801 CTCAGCGCGCTTACGCGGAGCTGATCCAGAAAGCGGCTTCGAGCTGCGCTGATCCGC 1860
QY 1861 CGCGCCACTCAGGCTACATGGACCGGCTCAACATGATACAGCTCTTCTACATGGCCGC 1920
Db 1861 CGCGCCACTCAGGCTACATGGACCGGCTCAACATGATACAGCTCTTCTACATGGCCGC 1920
QY 1921 CGGAAGGCGGCCAAGAGGACAACTAA 1947
Db 1921 CGGAAGGCGGCCAAGAGGACAACTAA 1947

RESULT 2
US-10-620-914-43
; Sequence 43, Application US/10620914
; Publication No. US20040093639A1
; GENERAL INFORMATION:
; APPLICANT: Benning, Christoph
; APPLICANT: Riekhof, Wayne
; APPLICANT: Klug, Rouven
; TITLE OF INVENTION: Compositions and Methods for the Production of Betaine Lipids
; FILE REFERENCE: MSU-07769
; CURRENT APPLICATION NUMBER: US/10/620,914
; CURRENT FILING DATE: 2003-07-16
; PRIOR APPLICATION NUMBER: 10/118,495
; PRIOR FILING DATE: 2002-04-08
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 43
; LENGTH: 5242
; TYPE: DNA
; ORGANISM: Chlamydomonas reinhardtii
US-10-620-914-43

Query Match 33.1%; Score 645; DB 7; Length 5242;
Best Local Similarity 100.0%; Pred. No. 2.4e-162;
Matches 645; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1045 CAGCTGTTGCGGAGGCGGTGCACCCCGCATTTGAGGAGCTGTACGAGAAGCTGGCG 1104
Db 3228 CAGCTGTTGCGGAGGCGGTGCACCCCGCATTTGAGGAGCTGTACGAGAAGCTGGCG 3287
QY 1105 CCCTTCCTGTGCGAAACAGGACCAACTTCTGTGTCGAAGCGCTCTGTACTTCCAGCAC 1164
Db 3288 CCCTTCCTGTGCGAAACAGGACCAACTTCTGTGTCGAAGCGCTCTGTACTTCCAGCAC 3347
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Db	242	CCTATCTCAGCAGGGCGGGCTCGATCCTCCCGTGGATCTCTCGCCGCGCCATGTGG	301
Qy	989	CGCTTCTGGAGCTCAAGAAAGTGGCCATTTCAGCAGCTG---GAGTTTGAAGAGCTGTGGC	1045
Db	302	CGCTGGGGCGCTGAAAGCTCGCCGCGCGGGACGCTGCCCGACCATGCCGCTTCTTCG	361
Qy	1046	AGCTGTTCCGGGAGGGCGTGCACCGCGGCAATTGAGAGCTGTACGAGAGAAGACTGGCGC	1105
Db	362	ATCTCTTCGGTTCGGCAGACCTCGCCGCGCAATCGGCGCCTTACGACCGGCCACATCGCGC	421
Qy	1106	CCTTCTCTGTCGCAAAACGAGCCACAACTTCTGTGTCCAAGCGCCTCTCGTATCTTCCAGCAGC	1165
Db	422	CCGCGCTCGACGCCGCGAGCCCGCGCTACTTGGGAGCGCGCAGCCCTTCGGCGCGCGCA	481
Qy	1166	GCCTGTACTACGAGGGCGGCGATGGGCAAGCTGTGTGGGTGCTGCAGTGCTCTGGCCG---	1222
Db	482	TCCAGCTGTTCGAGCGCGGCTTCTACCGGCACGGTGCCCTTCGGCCGCTTCATCGGCGGG	541
Qy	1223	-----TGTGTCTGGACTGGGCAAGACCGCTCAAGCGCCTCGCCAAACGCGCCCAACA	1273
Db	542	CCCATAGCTCGCGCGGGCGCGGCAACCGACCTGCGGGGCTTCTCGACTGTCTCCGACA	601
Qy	1274	TGAGAGAGCAGCCGCTCTGTGGGACAGCAATGCTCATCTCACTTCTGTGTGAAGAACGGGC	1333
Db	602	TCGAGGCGCAGCCAGCTTCTTCTAGCCGCATATCGGCGCGCTCTTCGAGGGCCCGGTGG	661
Qy	1334	CCAAGCGCTGTGTGGCTGTTCGTCAAGTTCTGTAGCCTGTGTGCTC	1380
Db	662	TGCAGGCGCTCGCCGACGCGCGCGCTCTTCGGGCTGGGGATC	708

RESULT 4
US-10-620-914-1
; Sequence 1, Application US/10620914
; Publication No. US20040093639A1

RESULT 3

```

; APPLICANT: Klug Rouven
; TITLE OF INVENTION: Compositions and Methods for the Production of Betaine L
; FILE REFERENCE: MSU-07769
; CURRENT APPLICATION NUMBER: US/10/620,914
; CURRENT FILING DATE: 2003-07-16
; PRIOR APPLICATION NUMBER: 10/118,495
; PRIOR FILING DATE: 2002-04-08
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 1252
; TYPE: DNA
; ORGANISM: Rhodobacter sphaeroides
US-10-620-914-1

Query Match 5.1%; Score 100.2; DB 7; Length 1252;
Best Local Similarity 50.9%; Pred. No. 2e-16;
Matches 299; Conservative 0; Mismatches 273; Indels 15; Gaps 2;

ov 809 TCCGCCCCACCTTCCTGTACAGCAGCTCTGTGGAGGACCCCGAGCCGGATATCGAGGTGA 868

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122	TCTTCACGGCTCGTCTATCCGACAGATCGGAGGATCCGCGGTGGACATGGGGCCCC	181
Db		
869	TGGAGATCAACCCCAAGGACACGGTGTCTACCTGACTAGCGCGGCTCGCAATGCCCTGA	928
Qy		
182	TGCCCATCGCCCGCCGGGACCGGTGGTGGCCATCGCTCGGGCGGTTGCAACGTGCTTT	241
Db		
929	ACTGCTGGTGCAGGGGGCCGCCAGGTGGTGTGGTGGACTGCACCCCGGCAGTCGG	988
Qy		
242	CCTATCTCAGCAGGGCGGGCTCGATCCTCGCGTGGATCTCTCGCCCGGCCCATGTGG	301
Db		
989	CGCTTCGTGAGCTGAAGAAGTGGGCCATTACGACGTG---GAGTTTAGAGAGGTGGC	1045
Qy		
302	CGTGGGGGGGTGAAGCTCGCGCCGCGCGAGACGTGCCGACCAATGCCGCTCTTCG	361
Db		


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; SEQ ID NO 48
; LENGTH: 3427
; TYPE: DNA
; ORGANISM: Neurospora crassa
US-10-620-914-48

Query Match      3.7%; Score 73; DB 7; Length 3427;
Best Local Similarity 51.0%; Pred. No. 4.8e-09;
Matches 172; Conservative 0; Mismatches 165; Indels 0; Gaps 0;

QY 779 ACAGGAGCGGTGGAGCGCGCCATGTTCCCGCCACCTTCTGTACAGCAGTCGT 838
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1906 AGGAGATCACTCCGAGACACCCAGTTCAATGACAGATACATCAGCCTTACT 1965
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 839 GGGAGAGCCCGAGCGCGATATGGAGTGATGGAGATCAACCCCAAGGACAGGTGCTGA 898
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1966 GGGAGAGCTCGCGCTCGACAGAGAACTCTTAACCTCGGGCCGACGAGTCGTCCTAG 2025
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 899 CCCTGACTAGCGCGGCTGCAATGCCCTGAACCTCTGTGTGAGGGCGCGCCAGGTGG 958
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 2026 CCATCACCAGCGCGCGGCGACAACTTCTTCTACCTGATGCAGAGTCCCGCTCGCGTGC 2085
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 959 TGTGGTGGAGTGCAACCCCGCGAGTCGGCGCTTCTGAGCTGAAGAAGTGGCCATTC 1018
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 2086 AGCCATGACTAAACCCAGCCAAACCCCTCTTGAATCAAGTCGCTCTTTTA 2145
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 1019 AGCAGCTGGAGTTTGAGGACGTGTGGCAGCTGTTCGGCGAGGGCGTGCACCCGCGCATTTG 1078
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 2146 CGACTCTGGATTACCCCGAGGTCTGGAAGATCTTCGGTGGGCAACACCCCGACTTTC 2205
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 1079 AGGAGCTGTACGAGAAGAGTGGCGGCTTCTGCTGTC 1115
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 2206 GCTCACTGCTATCTCCAAACTCTCCCTCACCTCTC 2242
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 8
US-10-481-112-1
; Sequence 1, Application US/10481112
; Publication No. US20040235721A1
; GENERAL INFORMATION:
; APPLICANT: WEBER, Olaf
; APPLICANT: FRIEDERICH, Sonja, Maria
; APPLICANT: SIEGLING, Angela
; APPLICANT: SCHLAPP, Tobias
; APPLICANT: MERCER, Andrew, Allan
; APPLICANT: FLEMING, Stephen, Bruce
; TITLE OF INVENTION: Recombinant proteins of Parapoxvirus ovis and pharmaceutical comp
; TITLE OF INVENTION: therefrom.
; FILE REFERENCE: Lea 35228
; CURRENT APPLICATION NUMBER: US/10/481,112
; CURRENT FILING DATE: 2003-12-12
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 137560
; TYPE: DNA
; ORGANISM: Parapoxvirus ovis NZ2
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (3)...(539)
; OTHER INFORMATION: ORF: L1
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (781)...(449)
; OTHER INFORMATION: ORF: L2r
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1933)...(1664)
; OTHER INFORMATION: ORF: L3r
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (3269)...(2790)
; OTHER INFORMATION: ORF: L4r
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (2799)...(3851)
; OTHER INFORMATION: ORF: L5
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (2962)...(3753)
; OTHER INFORMATION: ORF: L6
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (3784)...(3122)
; OTHER INFORMATION: ORF: L7r
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (4341)...(4129)
; OTHER INFORMATION: ORF: L8r
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (4904)...(4428)
; OTHER INFORMATION: ORF: L9r
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (6517)...(4970)
; OTHER INFORMATION: ORF: L1r
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (8042)...(6684)
; OTHER INFORMATION: ORF: L2r
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (9889)...(8070)
; OTHER INFORMATION: ORF: L3r
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (11195)...(10062)
; OTHER INFORMATION: ORF: L4r
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (11493)...(11227)
; OTHER INFORMATION: ORF: L5r
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (11802)...(12038)
; OTHER INFORMATION: ORF: L6
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (12358)...(12080)
; OTHER INFORMATION: ORF: L7r
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (13980)...(12364)
; OTHER INFORMATION: ORF: L8r
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (14826)...(14053)
; OTHER INFORMATION: ORF: L9r
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (15080)...(15394)
; OTHER INFORMATION: ORF: L10
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (16838)...(15423)
; OTHER INFORMATION: ORF: L11r
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (19021)...(16847)
; OTHER INFORMATION: ORF: L12r
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (19704)...(19156)
; OTHER INFORMATION: ORF: L13r
; FEATURE:
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; NAME/KEY: CDS
; LOCATION: (20314)...(19736)
; OTHER INFORMATION: ORF: 14r
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (20401)...(22101)
; OTHER INFORMATION: ORF: 15
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (22125)...(22940)
; OTHER INFORMATION: ORF: 16
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (23003)...(23866)
; OTHER INFORMATION: ORF: 17
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (26908)...(23873)
; OTHER INFORMATION: ORF: 18r
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (26926)...(27213)
; OTHER INFORMATION: ORF: 19
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (27626)...(27216)
; OTHER INFORMATION: ORF: 20r
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (29754)...(27616)
; OTHER INFORMATION: ORF: 21r
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (32217)...(29800)
; OTHER INFORMATION: ORF: 22r
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (33380)...(32418)
; OTHER INFORMATION: ORF: 23r
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (33602)...(33393)
; OTHER INFORMATION: ORF: 24r
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (34466)...(33612)
; OTHER INFORMATION: ORF: 25r
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (34735)...(34502)
; OTHER INFORMATION: ORF: 26r
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (35905)...(34739)
; OTHER INFORMATION: ORF: 27r
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (37194)...(35905)
; OTHER INFORMATION: ORF: 28r
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (37200)...(39248)
; OTHER INFORMATION: ORF: 29
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (41037)...(39229)
; OTHER INFORMATION: ORF: 30r
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (41374)...(42066)
; OTHER INFORMATION: ORF: 31
; FEATURE:
; NAME/KEY: CDS
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; LOCATION: (42336)...(41731)
; OTHER INFORMATION: ORF: 32r
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (42407)...(41997)
; OTHER INFORMATION: ORF: 33r
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (42410)...(43765)
; OTHER INFORMATION: ORF: 34
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (43770)...(43958)
; OTHER INFORMATION: ORF: 35
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (43980)...(44534)
; OTHER INFORMATION: ORF: 36

Query Match 3.7%; Score 72.4; DB 8; Length 137560;
Best Local Similarity 42.9%; Pred. No. 1.5e-08;
Matches 461; Conservative 0; Mismatches 611; Indels 2; Gaps 2;

Qy 618 CGACAACATTGACATCGGCCCGCGCGCTTCTGTGTACCTGGAGCAGAGCTGGAGCGGT 677
Db 20613 CGAGGTCTTCGACGCCGTGCTCAAGCGCGCTTCGACGCGCTCAGCTCTTTGTGCGGC 20672
Qy 678 GTGGAGCAGAACACCCAGGTTTCGATCCCTAGTCCGCTGGCTGGCGCCCTACTA 737
Db 20673 GCTCTCGCGCACTTCGAGGCTTCGTTGCCGCATCCGGCCCTACCGCGGACCTGCGC 20732
Qy 738 CGTGTGATTTGGCGCTGCCAGCGTTGGCCAGCCCTGCACGAGGAGCGCTGGAGCG 797
Db 20733 GGAGCTGCTGGCCGACGCGCGCTTCATGAGTGGTGGCGCGCGCGCGAGCTCGCGGA 20792
Qy 798 GCCGCCCATGTTCCCGCCCACTTCTGTGTACACGCACTGCTGGGAGGACCCCGAGCCGGA 857
Db 20793 GGTCAATTGGCGTGAACACGACATCGCGCGAACCCTCTTCGCGAGCGCGAGCCGT 20852
Qy 858 TATGAGGTGATGAGATCAACCCAAAGGACACGGTGTGTGACCTGTACTAGCGGGGCTG 917
Db 20853 GCGGAGCGGAGGCTCATTTTCGCAAGACCTTCGCAAGACCGAGTTCGCGCGCTCAA 20912
Qy 918 CAATGCCCTGAACCTGCTGGTGAGGGCGCGCGCGAGTGTGCTGGTGGACTGCAACC 977
Db 20913 GCGCTCGCGTGTGCGCTGTGTGTGTGGCTTCTCGTGAAGAGGACCTTGGCGG 20972
Qy 978 CGCGAGTTCGGCGCTTCTGGAGCTGAAGAAGGTGGCCATTTCAGAGCTGGAGTTGAGGA 1037
Db 20973 CGAGTACGCGGACAAACGACCGCCAGGACCTTTTACGCTGTGCAGAAAGCGCGGGGCC 21032
Qy 1038 CGTGTGCGAGCTGTTGCGGAGGCGGTGCACCGCGCATTCAGAGCTGTACGAGNAGAA 1097
Db 21033 CGTGGCCA-CAGCGCGCTCACAGAGCATTCGCGAGTACTCTTTCGCCGAGACAGCG 21091
Qy 1098 GCTGCGCCCTTCTGTGCAAAACAGCCACAACCTTCTGTGTCGAAGCGCCT-CTGGTACT 1156
Db 21092 CCAGCACTGGGTCTGGCTGAACCGCGCGGTGGCGAGCGAGAGGTGTACCGGACC 21151
Qy 1157 TCCAGCACGGCTTACTTACAGGGCGGCAATGGCAAGCTGTGTGGTGTGTGAGTGCC 1216
Db 21152 GGCCTCGCGCACGCTCTACGAGCGGTGTGCTAGCTACGCGTACTCAGAGGTCAAGCAGG 21211
Qy 1217 TGGCGGTGGTGGGACTGGGGAAGACCGTCAAGCGCTCGCCAAACGCGCCCAATGG 1276
Db 21212 GCGCGTGAACGCCAACACGCTCAAGCTCGTGTACCGGCTCGAGAGACCCCGACATCA 21271
Qy 1277 AGGAGCAGCGCGCTGTGTGGGACAGCAACATGCTCATCCACTTGTGAAGAACGGGCCA 1336
Db 21272 AGGCTGTGCTGACGCTCATCTACGACGTGCCGCGGACATCGTCGGCGCTCGTGACT 21331
Qy 1337 AGCGCTGGTGTGGCTGTTCGTTCAAGTTCGTGAGCGCTGGTGTCTTTCAAACAGGCGGTGC 1396
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Db 21332 CCGGAAACGAGGTGGCGGAGCTACTTCTGAGTCTGTACCGCGAGAACTTGTCTGACG 21391
Qy 1397 TGTGTTCCGCGCGCGCGTCCGGGCAAGCAGTACGCGCTGATCAAGCGGAGCGCATCC 1456
Db 21392 GACGCACTTACCTCGGACGCGCGCTTCCGGAGCAGACCTCTTCCGCGTGTGCGCGCG 21451
Qy 1457 CATTGAGAACTACATCGCGCGCACCATGAGCGGCTGGCGGAGAACTCGCAGTGGCGA 1516
Db 21452 TCGATCCGACTTCTTCGAGCCCGAGCGCATCCGGGAGGCTTTCAGCGCAGACGCGCGC 21511
Qy 1517 AGCAGAACTACTTCTACTACAACTGCCTCACCGGCAAGTCTCTCGCGCAACTGCCCCA 1576
Db 21512 TCGAGAGCGCTTACGAGCATGGACCTCAACAGCCCTCATGTGCGACCTCATCTAG 21571
Qy 1577 CTAATCGGAGCGCGCTTTCGCCACCTCAAGAGTGGCGTGGGACAACTTGACCG 1636
Db 21572 ACTCGTGGACCCCGACGCTGGCGCGCGGAGCGCGGCTGCACTGCGCGTGCAACAAG 21631
Qy 1637 TCTCCACCAACTTCTTCATGGAGGAGCTCAAGCGCGCACCTACACCAAGTGA 1690
Db 21632 AGGACTCCGACTACTTTCATCGGGAGTACACACCTACTCTTCTCTCAGCGAGA 21685

RESULT 9
US-10-118-495-32
; Sequence 32, Application US/10118495
; Publication No. US20030074688A1
; GENERAL INFORMATION:
; APPLICANT: Benning, Christoph
; APPLICANT: Riekhof, Wayne
; APPLICANT: Klug, Rouven
; TITLE OF INVENTION: Compositions and Methods for the Production of Betaine Lipids
; FILE REFERENCE: MSU-06897
; CURRENT APPLICATION NUMBER: US/10/118,495
; PRIOR FILING DATE: 2002-04-08
; PRIOR APPLICATION NUMBER: 60/283,812
; PRIOR FILING DATE: 2001-04-13
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 32
; LENGTH: 1251
; TYPE: DNA
; ORGANISM: Sinorhizobium meliloti
US-10-118-495-32

Query Match 3.6%; Score 70; DB 5; Length 1251;
Best Local Similarity 52.8%; Pred. No. 2.5e-08;
Matches 151; Conservative 0; Mismatches 135; Indels 0; Gaps 0;
Qy 806 TGTTCGCCGCCACCTTCTGTACAGCAGTGTGGGAGGACCCCGAGCGGATATGGAGG 865
Db 116 TGTCTTTTTCGGGACTCGTCTACCGCAGATCTGGGAGGACCCGATTGTGACATGGAG 175
Qy 866 TGATGGAGATCAACCCCAAGACACGGTGTGACCTACTAGCGGCGGCTGCAATGCC 925
Db 176 CGATGCAGATCCGTCGCCGACATCGGATCTGACGATCGGTTCGGCGGCTGCAACATGC 235
Qy 926 TGAACCTCTGTCGAGGGGCGCGCAGGTGTGTCGGTGGACTGCAACCCCGCGAGT 985
Db 236 TGACCTATCTCTCCCGAGCTGCGCGATAGAGTGTGATCTCAACCCCATCACA 295
Qy 986 CGGCGCTTCTGAGCTGAAGAGTGGCCATTTCAGCAGCTGGAGTTTGAGGACGTGTGGC 1045
Db 296 TCGGCTCAACCGGCTGAAGCTGTCTGCTTTTGGCCACTTCCGAGCCACAAGGACGTGG 355
Qy 1046 AGCTGTTTCGGCGAGGCGTGCACCGCGCATTTGAGGAGCTGTACGA 1091
Db 356 TCGGTTCTCTCGCGCTCGAAGGTACGCGACGAATGGCCAGCCTA 401

RESULT 10
US-10-620-914-32
; Sequence 32, Application US/10620914

; Publication No. US20040093639A1
; GENERAL INFORMATION:
; APPLICANT: Benning, Christoph
; APPLICANT: Riekhof, Wayne
; APPLICANT: Klug, Rouven
; TITLE OF INVENTION: Compositions and Methods for the Production of Betaine Lipids
; FILE REFERENCE: MSU-07769
; CURRENT APPLICATION NUMBER: US/10/620,914
; PRIOR FILING DATE: 2003-07-16
; PRIOR APPLICATION NUMBER: 10/118,495
; PRIOR FILING DATE: 2002-04-08
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 32
; LENGTH: 1251
; TYPE: DNA
; ORGANISM: Sinorhizobium meliloti
US-10-620-914-32

Query Match 3.6%; Score 70; DB 7; Length 1251;
Best Local Similarity 52.8%; Pred. No. 2.5e-08;
Matches 151; Conservative 0; Mismatches 135; Indels 0; Gaps 0;
Qy 806 TGTTCGCCGCCACCTTCTGTACAGCAGTGTGGGAGGACCCCGAGCGGATATGGAGG 865
Db 116 TGTCTTTTTCGGGACTCGTCTACCGCAGATCTGGGAGGACCCGATTGTGACATGGAG 175
Qy 866 TGATGGAGATCAACCCCAAGACACGGTGTGACCTACTAGCGGCGGCTGCAATGCC 925
Db 176 CGATGCAGATCCGTCGCCGACATCGGATCTGACGATCGGTTCGGCGGCTGCAACATGC 235
Qy 926 TGAACCTCTGTCGAGGGGCGCGCAGGTGTGTCGGTGGACTGCAACCCCGCGAGT 985
Db 236 TGACCTATCTCTCCCGAGCTGCGCGATAGAGTGTGTCATCAACCCCATCACA 295
Qy 986 CGGCGCTTCTGAGCTGAAGAGTGGCCATTTCAGCAGCTGGAGTTTGAGGACGTGTGGC 1045
Db 296 TCGGCTCAACCGGCTGAAGCTGTCTGCTTTTGGCCACTTCCGAGCCACAAGGACGTGG 355
Qy 1046 AGCTGTTTCGGCGAGGCGTGCACCGCGCATTTGAGGAGCTGTACGA 1091
Db 356 TCGGTTCTCTCGCGCTCGAAGGTACGCGACGAATGGCCAGCCTA 401

RESULT 11
US-10-118-495-22
; Sequence 22, Application US/10118495
; Publication No. US20030074688A1
; GENERAL INFORMATION:
; APPLICANT: Benning, Christoph
; APPLICANT: Riekhof, Wayne
; APPLICANT: Klug, Rouven
; TITLE OF INVENTION: Compositions and Methods for the Production of Betaine Lipids
; FILE REFERENCE: MSU-06897
; CURRENT APPLICATION NUMBER: US/10/118,495
; CURRENT FILING DATE: 2002-04-08
; PRIOR FILING DATE: 60/283,812
; PRIOR FILING DATE: 2001-04-13
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 22
; LENGTH: 1248
; TYPE: DNA
; ORGANISM: Mesorhizobium loti
US-10-118-495-22

Query Match 3.6%; Score 69.6; DB 5; Length 1248;
Best Local Similarity 45.0%; Pred. No. 3.1e-08;
Matches 500; Conservative 0; Mismatches 579; Indels 33; Gaps 5;
Qy 704 TCCCTACGTGCGCTGGCGGCGCCCTTACTACTGATGTGATTTGGCGGCTGCCAGCG 763
Db 11 TCTCTCGGATCTGTTTTCGCGCGGCAAGGAAGTTGGAAGGCGCTCTACCAGAAC 70

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QY 764 TTGGCCACGCGCTGCACGAGGAGCGGTGGAGCGCGCCGCAATGTTCCGCGCCACTTCC 823
Db 71 GCGCGCTTTCAAAGCCGGCATCTCCGAGCGGCTGTTCCGCTTCTCTGTTTTCGGGCTCG 130
QY 824 TGTACACGAGTCGTGGGAGGACCCCGAGCGCGATATGGAGGTGATGGAGATCAACCCCA 883
Db 131 TCTATCCGAGATCTGGGAAGACCCCGATGTCGACATGGAGGCCATGCAGCTTGTGTCAG 190
QY 884 AGGACACGGTGTGACCTGATAGCGCGGCTGCAATGCCCTGAACTGCTGTGTGTCAGG 943
Db 191 GCCATCGCATCGTCAACATCGTTCCGCGCGGTGCAACATCTCGCTACCTACCCGTT 250
QY 944 GGGCGGCGCAGTGTGTGCGTGACATGCAACCCCGCGCAGTCGCGCTTCTGGAGCTGA 1003
Db 251 CGCGCGGACGATACAGCGCGTGCACCTCAACCGCGCCCAATCGCGCTGAACCGCATGA 310
QY 1004 AGAAGGTGGCCATTGACGAGCTGGAAGTTTGAAGAGG---TGTGGCAGCTGTTCCGCGAGG 1060
Db 311 AGCTGGAGCGGTGCGCGTCTGCCCTCGAGGGCGATCTGTTCCGCTTTTCGGCGCG 370
QY 1061 GGTGCAACCGGCGATGAGAGCTGTACGAGAGAGCTGGCGGCTTCTCTGTGCGCAA 1120
Db 371 CCGACACGAGCCAAATTCGAAAGCCTATGACCGCTTTATTCGCGCGCATCTCGATCCGG 430
QY 1121 CCAGCCAACTTCTACAGACC---GSCCTGCTCGGCCCTGTTATCGCCATGGGCCATCGCA 547
Db 431 TCAGCGCGCATATTTGGGAGCGCGCAACTGGCGTGTGCGCGGCAATCGCGCTTCTCG 490
QY 1181 CGGCGATGGGCAAGCTGTGTGCGGTGTGTCAGTGTGCGCGCGTGTGTGGGACTGGGCA 1240
Db 491 ACCGCAATTTCTACAGACC---GGCGCTGCTCGGCGCTGTTTCCGCTTTTCGGCGCG 370
QY 1241 AGACCGTCAAGCGCTCGCCAAACCGGCCCAATGAGGAGGAGCAGCGCGCTGTGGGACA 1300
Db 548 CGGCGAAATTTCTTCAACGAGG-----AGCTGGCGCGGCTCTTCGACAAGA 652
QY 1301 GCAACATGCTCATCACTTCTGTAAGAAACGCGGCCCAAGCGCGCTGTGTGCTGTTCTG 1360
Db 608 AGCGCGGCTTCTTCAACGAGG-----AGCTGGCGCGGCTCTTCGACAAGA 652
QY 1361 AGTTGCTGAGCGCTGTGTGCTTCAACAGGCGGCTGTGTGTTCCGCGCGCGGCTGCGCG 1420
Db 1073 CAGGCGCGCGGCTCATCTTCGCGCACCGCGCGC 1104
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RESULT 12
US-10-620-914-22
; Sequence 22, Application US/10620914
; Publication No. US20040093639A1
; GENERAL INFORMATION:
; APPLICANT: Benning, Christoph
; APPLICANT: Riekhof, Wayne
; APPLICANT: Klug, Rouven
; TITLE OF INVENTION: Compositions and Methods for the Production of Betaine Lipids
; FILE REFERENCE: MSU-07769
; CURRENT APPLICATION NUMBER: US/10/620,914
; CURRENT FILING DATE: 2003-07-16
; PRIOR APPLICATION NUMBER: 10/118,495
; PRIOR FILING DATE: 2002-04-08
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 22
; LENGTH: 1248
; TYPE: DNA
; ORGANISM: Mesorhizobium loti
US-10-620-914-22

Query Match 3.6%; Score 69.6; DB 7; Length 1248;
Best Local Similarity 45.0%; Pred. No. 3.1e-08;
Matches 500; Conservative 0; Mismatches 579; Indels 33; Gaps 5;

QY 704 TCCCTAGTGTGCTGGTGGCGCGCCCTACTACGTGTGATTTGGCGGCTGCCACG 763
Db 11 TCTCTCGGATCTGTTTTCGCGCGGCAAGGAAGTTGGAAGCGCGCTTACCAGAAC 70
QY 764 TTGGCCACGCGCTGCACGAGGAGCGGTGGAGCGCGCCCATGTTCCGCGCCACTTCC 823
Db 71 GCGCGCTTTCAAAGCGGCGATCTCCGAGCGGCTGTTCCGCTTCTCTGTTTTCGGGCTCG 130
QY 824 TGTACACGAGTCGTGGGAGGACCCCGAGCGCGATATGGAGGTGATGGAGATCAACCCCA 883
Db 131 TCTATCCGAGATCTGGGAAGACCCCGATGTCGACATGGAGGCCATGCAGCTTGTGTCAG 190
QY 884 AGGACACGGTGTGACCTGACCTGACTAGCGCGGCTGCAATGCCCTGAACTGCTGTGTGTCAGG 943
Db 191 GCCATCGCATCGTCAACATCGCTTCCGCGCGCTGCAACATCTCGCTTCTACCCGTT 250
QY 944 GGGCGGCGCAGTGTGTGCGTGACCTGCAACCCCGCGCAGTCGCGCTTCTGGAGCTGA 1003
Db 251 CGCGCGGACGATCGACGCGCTGACCTCAACCGCGGCCAATCGCGCTGAACCGCATGA 310
QY 1004 AGAAGGTGGCCATTGACGAGCTGGAAGTTTGAAGAGG---TGTGGCAGCTGTTCCGCGAGG 1060
Db 311 AGCTGGAGCGGTGCGCGCTGCGCCCTCGCAGGGCGATCTGTTCCGCTTTTCGGCGCG 370
QY 1061 GGTGCAACCGGCGATGAGAGCTGTACGAGAGAGCTGGCGGCTTCTGTGCGCAA 1120
Db 371 CCGACACGAGCCAAATTCGCAAGCCTATGACCGCTTTATTCGCGCGCATCTCGATCCGG 430
QY 1121 CCAGCCAACTTCTGCTCCAAAGCGGCTTCTGTTACTTCCAGCAGCGGCTGTACTACAGG 1180
Db 431 TCAGCGCGCATATTTGGGAGCGCGCAACTGGCGTGTGCGCGGCGCATCGCGCTTCTCG 490
QY 1181 CGGCGATGGGCAAGCTGTGTGCGGTGTGTCAGTGTGCGCGCGTGTGTGGGACTGGGCA 1240
Db 491 ACCGCAATTTCTACAGACC---GGCGCTGCTCGGCGCTGTTTCCGCTTTTCGGCGCG 547
QY 1241 AGACCGTCAAGCGCTCGCCAAACCGGCCCAATGAGGAGGAGCAGCGCGCTGTGGGACA 1300
Db 548 CGGCGAAATTTCTTCAACGAGG-----AGCTGGCGCGGCTCTTCGACAAGA 607
QY 1301 GCAACATGCTCATCACTTCTGTAAGAAACGCGGCCCAAGCGCGCTGTGTGCTGTTCTG 1360
Db 608 AGCGCGGCTTCTTCAACGAGG-----AGCTGGCGCGGCTCTTCGACAAGA 652
QY 1361 AGTTGCTGAGCGCTGTGTGCTTCAACAGGCGGCTGTGTGTTCCGCGCGCGGCTGCGCG 1420
Db 1073 CAGGCGCGCGGCTCATCTTCGCGCACCGCGCGC 1104
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Db 653 ACCTTTTGAATGGGGACCTCGCTAAGGCTCTGCTGTTGGCTCGGCATTCGGCGG 712

Qy 1421 GCAAGAGTACCGCTGATCAAGGGCGGACGGCATCCCATTTAGAACTACATGCGCGCA 1480

Db 713 CGAGTACGATTCCCTGATCACTCAGGCGACGGCACCATGSCCAGCTTCTGAAGGCC 772

Qy 1481 CCATGGACGGCGTGGGAGAACTCGCAGTGGCGGCAAGCAGAACTACTTCTACTACACT 1540

Db 773 GGCTGGAAGAAGCTCGCTCGGATTTTCCTCCCTGGAAAAAAATATTTATTTCCGCTTGGCAGGCTT 832

Qy 1541 GCCTCAGCGCAAGTTCTCTGCGCAGCAACTGC-----CCACCTACTCTGGCGAGGGCG 1594

Db 833 TTGCGCGCGCTATCCAAATCCGCTGAGCGCGCGCTCTGCGCGCTATCTGGAAGCAGA 892

Qy 1595 CTTTCGCCACCT-----CAAGTGGGTGGTGGCAAACTGACCTGACCTTCTCCAACT 1648

Db 893 ACTAGAAACCATCCGCGCAATATCGACCGGTTCGCCATCCACATGCCAATCTGATCG 952

Qy 1649 TCTTCATGGAGGACTCAAGCGCGCACTACCAAGGTGATTTCTGATGGACACGTTGG 1708

Db 953 AATTCTCGCGCAAGGACGCGGCACTGATCGATCGCTTTCATCTGCTCGATGCGCAGG 1012

Qy 1709 ACTGCTGATATCCGTTGGCGCAAGAGCTGGCGAGTGCCTGSCCAAGCAGGTTGGC 1768

Db 1013 ACTGATGACCGATGACAGCTCAAGCGCTGTGTGCGAAATCAGCGCGCTCG 1072

Qy 1769 CGGCGCGCATCTATCTGGGCTCCGCTCC 1800

Db 1073 CAGGCGCGGCTCATCTTCGCGACGCGCGC 1104

RESULT 13

US-10-204-434A-12

; Sequence 12, Application US/10204434A

; Publication No. US20030170662A1

; GENERAL INFORMATION:

; APPLICANT: SETO, Haruo

; APPLICANT: KUZUYAMA, Tomohisa

; TITLE OF INVENTION: A Method For Screening A Substance Which Specifically Inhibits No

; TITLE OF INVENTION: Mevalonate Pathway

; FILE REFERENCE: P22747

; CURRENT APPLICATION NUMBER: US/10/204,434A

; CURRENT FILING DATE: 2002-08-30

; PRIOR APPLICATION NUMBER: PCT/JP01/01501

; PRIOR FILING DATE: 2001-02-28

; NUMBER OF SEQ ID NOS: 15

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 12

; LENGTH: 1104

; TYPE: DNA

; ORGANISM: Streptomyces sp.

US-10-204-434A-12

Query Match 3.5%; Score 67.8; DB 6; Length 1104;

Best Local Similarity 45.1%; Pred. No. 9.3e-08;

Matches 252; Conservative 0; Mismatches 307; Indels 0; Gaps 0;

Qy 1344 GGTGTGGCTGTTCTGTCAGTTTCGTGAGCTGCTGCTCTTCAACAGGCGGCTGTGTGTT 1403

Db 513 GGTCCCGAGATCGAAGATCGCGGCGCGTGCACATCCCCGTGATCTGTCAGGAGGT 572

Qy 1404 CGGCGCGGCGTGGCGGCAAGCAGTACGCGCTGATCAAGGCGGACGGCATCCCCATTGA 1463

Db 573 CGGCAAGGCTTGAAGCAGACCATCTGCTGCTCGCGACCTCGCGGTGCAGGCGG 632

Qy 1464 GAATACATCGCGGCACATGGACGGGTGGGAGAACTCGACAGTGGCGGAGCAGAA 1523

Db 633 GGAGTCAGCGCGCGCGGCGCAGGACTTCGCGCGCATCAGAAACGCGCGCGGAGCT 692

Qy 1524 CTACTTCTACTACAACTGCCTCACCGGCAAGTTCTGCGCGCAGCAACTGCCCCACCTACT 1583

Db 693 CGGCGACTACGGTTCTTGACGGGTGGGGGAGTTCACACCGCGCGCTGCTGCGGACG 752

Qy 1584 GCGGAGCGGCGCTTCGCCACCCCTCAAGAGTGGCGTGGTGAACAACCTGACCGTCTCCAC 1643

Db 753 CCAGGACATCTCCCTGCGCGCTCTCGCTCGCGCGGTGTGCGTCAACCGCTCGACGTGGT 812

Qy 1644 CAATTTTCATGAGGAGCTCAAGAGCGGCACCTACACCAAGGTGATTTCTGATGGACCA 1703

Db 813 CGGCGCTTCGGCTCGCGCGCGCGCGCTCGGCTCTCCCGCGGCTTCCTGCGCACCT 872

Qy 1704 CGTGGACTGGTGATATGCCGCTGGCCGCAAGCTGGCTGGCTGGCTGGCTGGCTGGCT 1763

Db 873 GATGACGACGCGCTCGACGCGCTGATCAAGAAGCTCAGGACCTGGCTGGACCGACTGGC 932

Qy 1764 TGCGCGGCGGCGCTGCTGCTGCGCTCGCGCTCTCCCTCAGCGCGCGCTAGCGGAGCT 1823

Db 933 GCGCTGCGACCATGCTGCGCGCGCGCACCCCGCGCGACCTCACCGCTGCGAGTGT 992

Qy 1824 GATCCAGAAGCGGCTTCGAGCTGCGTGCATCCGCGCGCGCACTCAGGGGTATACATGA 1883

Db 993 GCTCCAGCGAGCTGCGTGAATTTCTGCGCGCATCGGGGCGATCGACGCGCGCTCGC 1052

Qy 1884 CCGGCTCAACATGTACAGC 1902

Db 1053 CCAGCGCTCCAGCTCCATC 1071

RESULT 14

US-09-918-740-57

; Sequence 57, Application US/09918740

; Publication No. US20030033626A1

; GENERAL INFORMATION:

; APPLICANT: Hahn, Frederick

; APPLICANT: Kuehnle, Adelheid

; TITLE OF INVENTION: Manipulation of genes of the mevalonate and isoprenoid pathways t

; TITLE OF INVENTION: create novel traits in transgenic organisms

; FILE REFERENCE: KAS-103XCI

; CURRENT APPLICATION NUMBER: US/09/918,740

; CURRENT FILING DATE: 2001-07-31

; PRIOR APPLICATION NUMBER: 60/221,703

; PRIOR FILING DATE: 2000-07-31

; NUMBER OF SEQ ID NOS: 76

; SOFTWARE: Patent in version 3.0

; SEQ ID NO 57

; LENGTH: 6798

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Streptomyces sp Cll190 gene cluster containing mevalonate pathway

; OTHER INFORMATION: and lpp isomerase orfs

US-09-918-740-57

Query Match 3.5%; Score 67.8; DB 3; Length 6798;

Best Local Similarity 45.1%; Pred. No. 1.4e-07;

Matches 252; Conservative 0; Mismatches 307; Indels 0; Gaps 0;

Qy 1344 GGTGTGGCTGTTCTGTCAGTTTCGTGAGCTGCTGCTCTTCAACAGGCGGCTGTGTGTT 1403

Db 3835 GGTCCCGCAGATCGAAGATCGCGGCGCGCTGCACATCCCCGTGATCTGTCAGGAGGT 3894

Qy 1404 CGGCGCGGCGTGGCGGCAAGCAGTACGCGCTGATCAAGGCGGACGGCATCCCCATTGA 1463

Db 3895 CGGCAAGCGCTGAGCGCGCGCGCACCGACTTCGCGCGCATCGAGAAGCGCGCGGAGCT 3954

Qy 1464 GAATACATCGCGGCACCATGAGCGGCTGGCGGAGAACTCGACAGTGGCGGAGCAGAA 1523

Db 3955 GGAGCTCAGCGCGCGCGCGCGCACCGACTTCGCGCGCATCGAGAAGCGCGCGGAGCT 4014

Qy 1524 CTACTTCTACTACAACTGCTCAGCGGCAAGTTCCTGGCGGACAACTGCCCGCCACTTACT 1583

Db 4015 CGGCGACTACGCGTCTCTGCAAGGCTGGGCGGCGAGTTCACCGCGCGCTGCTGTGGACG 4074

Qy 1584 GCGGAGGCGGCGCTTCGCCACCCCTCAAGAGTGGGTGGTGGAGCAACCTGACCGTCTCCAC 1643

Db 4075 CCAGGACATCTCCCTGCGCGCTTCGCGCTCGCGCGGTGTGCGTCAACCGCTCGACGTGGT 4134

QY 1644 CAACTTCTTCATGAGGAGCTCAAGCGCGACCTACACCAAGTGATTCTGATGGACCA 1703
 Db 4135 CCGCGCCCTCGCGCTCGCGCGCCCGCGCTCGGCTCCCTCCGCGGCTTCTTGGCAGCCCT 4194
 QY 1704 CGTGACTGGCTGGATATGCCGCTGGCCCAACGAGCTGGCGGAGTGCCTTGGCCCAAGCAGGT 1763
 Db 4195 GATGGACGACGGCTGCGAGCGGCTGATCAGAGCTCAGACCTGGCTGGACCAAGCTGGC 4254
 QY 1764 TCGCGCGCGCGGATCGTCAATCTGGCGCTTCGCGCTCCCTCAGCGCGGCTTACGCGGAGCT 1823
 Db 4255 GCGGCTGCGAGCACTGCTCGGCGCGCGCACCGCGCGGACCTCACCGCTGCGAGCTGCT 4314
 QY 1824 GATCCAGAAGCGGGCTTCGAGCTGCGCTGCTATCGCGCGGCGGCTCAGGGCTACATGGA 1883
 Db 4315 GCTCCACGGCGAGCTGCGTGACTTCTGCGCGGACCGGGGCGATCGACACGCGCGGCTCGC 4374
 QY 1884 CCGCGTCAACATGTACAGC 1902
 Db 4375 CCAGCGCTCCAGCTCCATC 4393

RESULT 15
 US-10-204-434A-13
 ; Sequence 13, Application US/10204434A
 ; Publication No. US20030170662A1
 ; GENERAL INFORMATION:
 ; APPLICANT: SETO, Haruo
 ; APPLICANT: KUZUYAMA, Tomohisa
 ; TITLE OF INVENTION: A Method For Screening A Substance Which Specifically Inhibits No
 ; TITLE OF INVENTION: Mevalonate Pathway
 ; FILE REFERENCE: P22747
 ; CURRENT APPLICATION NUMBER: US/10/204,434A
 ; CURRENT FILING DATE: 2002-08-30
 ; PRIOR APPLICATION NUMBER: PCT/JP01/01501
 ; PRIOR FILING DATE: 2001-02-28
 ; NUMBER OF SEQ ID NOS: 15
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 13
 ; LENGTH: 6798
 ; TYPE: DNA
 ; ORGANISM: Streptomyces sp.
 US-10-204-434A-13

Query Match 3.5%; Score 67.8; DB 6; Length 6798;
 Best Local Similarity 45.1%; Pred. No. 1.4e-07;
 Matches 252; Conservative 0; Mismatches 307; Indels 0; Gaps 0;

QY 1344 GGTGTGGCTGTTTCGTCAAGTTTCGTGAGCTGCTGCTCTTCAACAGGCGGCTGTGTGTT 1403
 Db 3835 GGTCCCGCAGATCGAAGATCGCGGCGGCTCGACATCCCGTGATCGTCAAGGAGGT 3894
 QY 1404 CGGCGCGCGCTGCGGCGCAAGAGTACGCGCTGATCAAGGCGGACCGCATCCCATTTGA 1463
 Db 3895 CGGCAACGGCTGAGCCGGCAGACCATCTGCTGCTCGCGACCTCGGCGTGCAGGCGGC 3954
 QY 1464 GAACTACATCGCGCGCACCATGGAGCGGCTGGCGGAGAACTCGACAGTGGCGCAAGCAA 1523
 Db 3955 GGACGTACAGCGCGCGCGCGCAAGGACTTCGCCCGCATCGAGAACGCGCGCGGGAGCT 4014
 QY 1524 CTACTTCTACTACAACTGCCTCACCGCAAGTTCTCGCGGACAACTGCCCCACCTAGCT 1583
 Db 4015 CGGCGACTACGGGTTCTGTGACGGCTGGGGGAGTCCACCGCGGCTGCTGTGGACGC 4074
 QY 1584 CGCGAGGCGGCTTTCGCCACCTCAAGAGTGGCGTGGTGAGCAACCTGACCGTCTCCAC 1643
 Db 4075 CCAGGACATCTCCCTGCGCGCTCTCGCTCGCGGCGTGTGCTACCGGCTCGACGTGGT 4134
 QY 1644 CAACTTCTTCATGAGGAGCTCAAGCGGCGGACCTACACCAAGTGATTCTGATGGACCA 1703
 Db 4135 CCGCGCCCTCGCGCTCGCGCGCGCGGCTCGGCTCCCTCCGCGGCTTCTTGGCAGCCCT 4194
 QY 1704 CGTGACTGGCTGGATATGCCGCTGGCCCAAGAGCTGGCGGAGTGCCTTGGCCAAAGCAGGT 1763

Db 4195 GATGGACGACGGCTTCGAGCGGCTGATCAGAAAGTCAAGACCTGAGCTGGCTGGACCAAGCTGGC 4254
 QY 1764 TCGCGCGCGGCGGATCGTCAATCTGGCGCTTCGCGCTCCCTCAGCGCGGCTTACGCGGAGCT 1823
 Db 4255 GCGGCTGCGAGCACTGCTCGGCGCGCGCACCGCGCGGACCTCACCGCTGCGAGCTGCT 4314
 QY 1824 GATCCAGAAGCGGGCTTCGAGCTGCGCTGCTATCGCGCGGCGGCTCAGGGCTACATGGA 1883
 Db 4315 GCTCCACGGCGAGCTGCGTGACTTCTGCGCGGACCGGGGCGATCGACACGCGCGGCTCGC 4374
 QY 1884 CCGCGTCAACATGTACAGC 1902
 Db 4375 CCAGCGCTCCAGCTCCATC 4393

Search completed: May 4, 2006, 19:49:06
 Job time : 1624 secs

GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: May 4, 2006, 18:09:12 ; Search time 363 Seconds
(without alignments)
9534.194 Million cell updates/sec

Title: US-10-620-914-44

Perfect score: 1947
Sequence: 1 atggggctgggtcgtgacgg.....gcgccaagaaggacaactaa 1947

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : Issued Patents NA.*
- 1: /cgn2_6/ptodata/1/ina/1 COMB.seq.*
 - 2: /cgn2_6/ptodata/1/ina/5 COMB.seq.*
 - 3: /cgn2_6/ptodata/1/ina/6A COMB.seq.*
 - 4: /cgn2_6/ptodata/1/ina/6B COMB.seq.*
 - 5: /cgn2_6/ptodata/1/ina/H COMB.seq.*
 - 6: /cgn2_6/ptodata/1/ina/PTTUS COMB.seq.*
 - 7: /cgn2_6/ptodata/1/ina/PP COMB.seq.*
 - 8: /cgn2_6/ptodata/1/ina/RE COMB.seq.*
 - 9: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	69.4	3.6	3003	3	US-09-252-991A-14790
2	69.4	3.6	3132	3	US-09-252-991A-14540
3	69.4	3.6	3411	3	US-09-252-991A-14823
4	68.2	3.5	2830	2	US-09-010-928B-1
5	63	3.2	1691	3	US-09-902-540-6564
6	63	3.2	2034	3	US-09-902-540-8514
7	63	3.2	2730	3	US-09-902-540-489
8	63	3.2	1082	3	US-09-881-165-4
9	62.4	3.2	1167	3	US-09-902-540-2993
10	62.4	3.2	1250	3	US-09-902-540-362
11	62.4	3.2	1259	3	US-09-902-540-7318
12	62.2	3.2	3579	3	US-09-902-540-694
13	62.2	3.2	5656	3	US-09-902-540-6237
14	61.8	3.2	981	3	US-09-902-540-1047
15	61.8	3.2	1332	3	US-09-902-540-1164
16	61.8	3.2	19726	3	US-09-969-852-4
17	61.6	3.2	1852	3	US-09-902-540-7495
18	61.4	3.2	1281	3	US-09-902-540-726
19	61.4	3.2	6269	3	US-09-902-540-10513
20	60.8	3.1	951	3	US-09-252-991A-10546
21	60.8	3.1	1653	3	US-09-252-991A-10316
22	60.8	3.1	1701	3	US-09-252-991A-10316
23	60.4	3.1	1515	3	US-09-902-540-9184
24	60.4	3.1	9556	3	US-09-902-540-982

c	25	60.2	3.1	1563	3	US-09-902-540-8878	Sequence 8878, Ap
	26	60.2	3.1	10528	3	US-09-902-540-945	Sequence 945, App
	27	60	3.1	9818	3	US-09-902-540-987	Sequence 987, App
	28	59.6	3.1	1941	3	US-09-902-540-6922	Sequence 6922, Ap
	29	59.6	3.1	4359	3	US-09-902-540-594	Sequence 594, App
	30	59.2	3.0	1773	3	US-09-902-540-7746	Sequence 7746, Ap
	31	59.2	3.0	4854	3	US-09-902-540-768	Sequence 768, App
	32	58.8	3.0	1293	3	US-09-902-540-6161	Sequence 6161, Ap
c	33	58.8	3.0	1675	3	US-09-902-540-302	Sequence 302, App
c	34	58.4	3.0	1011	3	US-08-252-991A-12311	Sequence 12311, A
	35	58.4	3.0	1236	2	US-08-440-856A-1	Sequence 1, Appli
	36	57.8	3.0	1526	3	US-09-902-540-5594	Sequence 5594, Ap
c	37	57.8	3.0	41927	3	US-09-902-540-1268	Sequence 1268, Ap
	38	57.6	3.0	4345	3	US-09-949-016-2755	Sequence 2755, Ap
	39	57.6	3.0	8346	3	US-09-949-016-14497	Sequence 14497, A
	40	57.4	2.9	975	3	US-09-365-150-3	Sequence 3, Appli
	41	57.4	2.9	2261	3	US-09-158-767-1	Sequence 1, Appli
	42	57.4	2.9	2261	3	US-09-713-794-1	Sequence 1, Appli
c	43	57.4	2.9	9191	3	US-09-902-540-918	Sequence 918, App
	44	57	2.9	1059	3	US-09-252-991A-7911	Sequence 7911, Ap
	45	57	2.9	1338	3	US-09-252-991A-7764	Sequence 7764, Ap

ALIGNMENTS

RESULT 1
US-09-252-991A-14790
; Sequence 14790, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 14790
; LENGTH: 3003
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-14790

Query Match		3.6%	Score 69.4;	DB 3;	Length 3003;
Best Local Similarity		43.8%	Pred. No. 0.00015;		
Matches 454;		Conservative 0;	Mismatches 571;	Indels 12;	Gaps 3;
Qy	521	TGGCGGTTGCCGACTTCTAGCTGAGCGCAAGTACGACCTGCCCTCGCCGAGATGCCCT	580		
Db	1965	TGGCGGTCGAGCGGAGCAACCCGACCTCAACCGCGCGCTGCTGATCACTCAAGC	2024		
Qy	581	GGTCGCGCCGTTTCTTCTGCGCATCGATCTTCGACATCGAACATTCGACATCGCCCGC	640		
Db	2025	CGCACGGAGCGCGAGCTCACCGCAGGAGTATCCAGCGCTGCAGCCGCACTCG	2084		
Qy	641	AGCCCGCGGCTTACCTGGAGCAGAGCTGAGCGCGTGTGGGAGCAGACACCCAGGTT	700		
Db	2085	ACCACTGCCCGGGATCAAGCTGTACATGACGCGGTGCAGGACCTGACCATCGAGGACC	2144		
Qy	701	CGATCCCTAGTGGCGTGGCTGCGCCCTACTAGTGTGGATGGCGGCTGCCCA	760		
Db	2145	GGGTGCGCGGACCCAGTACACAGTTACCTTGCAGGACCGCGACCGGAGCTGTTCGCGG	2204		
Qy	761	CGGTTGGCCACGCCCTGCAGGAGCGCGGTGGAGCGCGCCCTGTTCCCGCCCACT	820		
Db	2205	AGTGGGTGCGGAGCTGGTGGCGGCTGCAGGAGTGGCGGAGTTCGCGCAGCTCGCCGACGTCGCA	2264		
Qy	821	TCCTGTACAGCAGTCTGTGGAGGAGCCCCGAGCCGGATATGGAGGTGATGGAGATCAACC	880		


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QY 1538 ACTGCCTCACCAGCAAG 1554
Db 2810 ACCGCAACGAAGCAAG 2826

RESULT 3
US-09-252-991A-14823/c
; Sequence 14823, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 14823
; LENGTH: 3411
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-14823

Query Match 3.6%; Score 69.4; DB 3; Length 3411;
Best Local Similarity 43.8%; Pred. No. 0.00015;
Matches 454; Conservative 0; Mismatches 571; Indels 12; Gaps 3;

QY 521 TGGGGTTCGCGACTTCTACGTGAGCGGCAAGTACGACCTGCCCTCGCCAGATGCCCC 580
Db 1349 TCGCGTTCGCGAGCGAGCAACCGACCTCAACACCGCGCGCTGTGTATCAACCTCAAGC 1290
QY 581 GGTGCGCGCTTCTTCTGCGGATCGATCTTCGACATCGACAACATTGACATCGGCCCG 640
Db 1289 GCGACAGGAGCGGACGTCAACCGCAGGAAGTATCCAGGCTCGAGCCGCAACTCG 1230
QY 641 AGCGCGCGCTTACTCTGAGCAGAGCTGGAGCGCGTGTGGAGCAGAACACCCAGGGTT 700
Db 1229 ACCACCTGCCGGGATCAAGCTGTATCATGACGCGGTGCAGGACCTGACCATCGAGACC 1170
QY 701 CGATCCCTTACGTGCGGTGCGCGCCCTTACTAGTGTGATGTTGGCGCTGCGCCA 760
Db 1169 GGGTGGCGCGCACCGACGTACAGTTTCACTTTCAGGACGCGCGACCGTGTGCGCG 1110
QY 761 GCGTTGGCCACGCTGACAGGAGCGGTGGAGCGCGCTGTCGCGCCCTTCTCCGCGCACT 820
Db 1109 AGTGGGTGCGAAGCTGGTGGCGCGGTGCGAGAGTTGCGCGACGTGCGCGACGTGCGCA 1050
QY 821 TCCTGTATACACGACGTGCTGGGAGGACCCCGAGCGCGATATGAGGTGATGGAGATCAACC 880
Db 1049 GCGACTGGCAGGACAGGGCTTGAGGCTTACTGACATCGACGCG------ACACCG 996
QY 881 CCAAGGACCGGTGTGACCTGACTAGCGCGCTGCAATGCCCTGAACCTGTGTGTC 940
Db 995 CCTGCGCGCTCGCGGTGAAGCTCTCCGACATCGACAGCGTCTCTACAACGCTTCGCGC 936
QY 941 AGGGGGCGCGCAGGTGGTGTGCGTGGACTGCAACCCCGCGCATGTCGGCGCTTCTGGAGC 1000
Db 935 AGCGGTGATCTGACCATCTTCAACCCAGGCGCACCCAGTACCGCGTGGTGTGAGGTGG 876
QY 1001 TGAAGAAGGTGGCCATTGACGAGCTGGAGTTTGAAGGACGTGTGGCAGCTGTTCCGCGAGG 1060
Db 875 GCGCGAGTTCAGCTCGGCGCGCGAGGCTTGAGGACGTCTAGTCCGCTCGAGCGAGC 816
QY 1061 GCGTGCACCCCGCATGAGAGCTGTACGAGAAGAGCTGGCGCCCTTCTGTGCAAA 1120
Db 815 GCACCCAGGTGCGCTGTGCGAGCTTGGCGAAGGTGGAGGAGCGGCATACCTGTGCGGA 756
QY 1121 CCAGCCCAACTTCTGTGTCGAAGCGCTCTGTGTACTTCCAGCAGGCGCTGTACTACGAG 1180
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Db 755 TCAACCATATCGCCAGTTC---CCCTCGdCGAACCCCTGTGTCTTCAACTGGCCAAAGGGTT 699
QY 1181 GCGGCATGGCAAGCTGTGCTGGGTGTGdAGTGTCTGCGCGGTGTGTGTGGACTGGGCA 1240
Db 698 ACTCCTGGGCGAGGCGGTTCGAGGCGATCCGCTGGCGTTCGAGGCCAGCCTGGAGCTGCCGC 639
QY 1241 AGACGGTCAAGGGCTTCGCAACGGGCCCAANTGGAGGAGAGCGCGCTGTGTGGACA 1300
Db 638 TGAGCATGCAAGGAGCTTCGCGCGCGCGGCGCTTTCGAGGCCCTCGCTGTGCAACA 579
QY 1301 GCAACATGCTCATCC---ACTTCTGTGAAGAAGCGGCCCAAGCCGTGTGTGGCTGTTCG 1357
Db 578 CGTGTCTCTGATCTCGCTCTGCTGCTGAGCATGTACATGTCTCTGGGCATCTCTCTAG 519
QY 1358 TCAAGTTCTGTGAGCTGTGTCTCTTCAACAAGGCGCTGTGTGTTCGGCGCGCGCTGC 1417
Db 518 AGAGCTTCATCCATCCGCTGACCATCTCTCTGACCCCTGCGCCCTCGCGCGGGTTCGCGCGC 459
QY 1418 CGGCAAGCAGTACGCGCTGATCAAGCGGAGCGGATCCCCATTTGAGAACTATACATCGCGC 1477
Db 458 TGCTGGCGCTGATGTGCGCGGCGAGGATCGGCATCGTGGCGATCATCGGCATCATCC 399
QY 1478 GCACCATGGAGCGGTGCGGAGAACTCGCACGTGCGCAAGCGCATATGATCATGATCGACTTCCCTTCGACGCGC 1537
Db 398 TGCTGATCGGCATCGTCAAGAAGAAGCGGCATATGATCATGATCGACTTCCCTTCGACGCGC 339
QY 1538 ACTGCTTCACCGGCAAG 1554
Db 338 AGCGCAACGAAGGCAAG 322

RESULT 4
US-09-010-928B-1
; Sequence 1, Application US/09010928B
; Patent No. 5994099
; GENERAL INFORMATION:
; APPLICANT: Lewis, Randolph V
; APPLICANT: Hayashi, Cheryl Y
; TITLE OF INVENTION: EXTREMELY ELASTIC SPIDER SILK PROTEIN AND DNA
; TITLE OF INVENTION: CODING THEREFOR
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH
; STREET: 8110 GATEHOUSE RD. SUITE 500E
; CITY: FALLS CHURCH
; STATE: VIRGINIA
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 22042
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/09/010,928B
; APPLICATION NUMBER: US/09/010,928B
; FILING DATE: 22-JAN-1998
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Murphy Jr., Gerald M
; REGISTRATION NUMBER: 28977
; REFERENCE/DOCKET NUMBER: 1447-109P
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2830 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; FEATURE:
; NAME/KEY: -
; LOCATION: 1..2830
; OTHER INFORMATION: /note= "Flagelliform DNA sequence"
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OTHER INFORMATION: taken from the 5' region. The putative start codon is at
OTHER INFORMATION: position 219"

FEATURE:
NAME/KEY: CDS
LOCATION: 219..2830
US-09-010-928B-1

Query Match 3.5%; Score 68.2; DB 2; Length 2830;
Best Local Similarity 46.4%; Pred. No. 0.00025;
Matches 290; Conservative 0; Mismatches 333; Indels 2; Gaps 2;
Qy 772 GCCCTTGACAGGAGCGGTGGAGCGCGCCCTGTTCCCGCCACCTTCTCTGTACACG 831
Db 1033 GACCTGGTGAGCCGGACACGAGGTATGACCTGTGTGGAGCCGGACGAGGATTACG 1092
Qy 832 CAGTCGTGGGAGGACCCCGACCGGATATGAGGTGATGAGATCAACCCCAAGACACG 891
Db 1093 GACCTGGTGAGCTGGACACGAGGATTACGACCTGTGTGAGCTGGGCTTGGAGTTACG 1152
Qy 892 GTGCTGACCTGACTAGCGGCGGCTGCATGCCCTGAACTGCTGTGTGCAGGGGCGCGC 951
Db 1153 GACCTGTGTGAGCTGGACCTGGAGGTTACGACCTGTGTGAGCTGGACCTGGAGTTACG 1212
Qy 952 CAGGTGTGTGCTGGGACTGCAACCCCGCAGTCGGCGCTTCTGGAGCTGAAGAAGTG 1011
Db 1213 GACCTGTGTGAGCTGGACCTGTGTGATACGACCTGTGTGAGCTGGACCTGGAGGTTG 1272
Qy 1012 GCCATTACGAGCTGGAGTTTGGAGACGTGTGGAGCTGTTCCGGAGGGCGTGACCCG 1071
Db 1273 GACCTGGAGGAGCTGGACACGAGGATATGACCTGTGTGTGCTGGACCTGTGTGTGCTG 1332
Qy 1072 CGCATTTAGGAGCTGTACGAGAAAGCTGGCGCCCTTCTTG-TCGAAACACGCCACAA 1130
Db 1333 GACCTGTGTGTGCTGGACCTGTGTGTGACCTGTGTGTGCTGGACCTGTGTGTGCTG 1392
Qy 1131 CTTCTGTGTCGAAGCGCTCTGTACTTCCAGCAGCGCTGTACTACAGGGCGGATGGG 1190
Db 1393 GACCTGTGTGATACGGCTCTGTGTGATCTGACCTGTGTGTGCTGGACCTAGTGTGCGC 1452
Qy 1191 CAACTGTGTGTGTGTGTGAGTGCCTGGCGGTGTGTGGACTGTGGGCAAGACGTCAC 1250
Db 1453 GACTTGTGTGT-GCTGGACCTGGAGTGCAGGCTTGGTGAGCAGGACCTTGGAGGAC 1511
Qy 1251 CGGCTGCGCAACGGCCCAATAGGAGGACGCGCGCTGTGTGGACAGCAACATGCT 1310
Db 1512 GGAACCACTGTGTGCGGACCCGGTGTGAGCAGGA CCGGTGTGAGCAGGACAGGTGATGCT 1571
Qy 1311 CATCCACTTCGTGAAGAACCGGCGCCCAAGCCGCTGTGTGTGCTGTTCGTCAAGTTCTGTGAG 1370
Db 1572 GGACCGGTGTGTGAGGACGTGGAGGACAGGTCTGTGTGTGTGTGTGTGTGTGTGTGCA 1631
Qy 1371 CCTGTGTCTTCAACAGGCGGTG 1395
Db 1632 GGTGTGTGAGGTGCAGGACGTGGTG 1656

RESULT 5
US-09-902-540-6564
; Sequence 6564, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 6564

LENGTH: 1691
TYPE: DNA
ORGANISM: Myxococcus xanthus
US-09-902-540-6564
Query Match 3.2%; Score 63; DB 3; Length 1691;
Best Local Similarity 44.9%; Pred. No. 0.0024;
Matches 323; Conservative 0; Mismatches 390; Indels 6; Gaps 2;
Qy 659 AGCAAGCTGAGCGGTGTGGAGCAGAAACCCAGGGTTCATCCCTACGTGCGGT 718
Db 260 AGGTGCGGCTGGCCACCGCTGGCGCGAAGCTGCCCAACGGCATGACATCAAGACGGCG 319
Qy 719 GGCTGCGCGCCCTTACTAGTGTGGATTGSCCGCTGCCAGGTTGGCCACGCCCTGCG 778
Db 320 CGCTGCGCGGCTGGACAGCTTCCGATGCTCTGCTGTCCA---AGGAGTGGCGCTGA 376
Qy 779 ACAGGAGCGGTGTGGAGCGCGCCCATGTTTCCGCCCCACCTTCTGTACACGAGTCTG 838
Db 377 GCGAGGAGTCCAGCGGCTGCTCATCTTCCGGCGGACACGCGGTGGGCACGCCCATCG 436
Qy 839 GGGAGGACCCCGACCGGATATGAGGTGATGAGATCAACCCCAAGACACGGTGTGTA 898
Db 437 CGGAGGCGGTGGGCTGGATGGCGTGTGTGTGGAGGTGAACGTCAACCCGAACCGCCCG 496
Qy 899 CCCTGACTAGCGGCGGTGCAATGCCCTGAACTGCTGTGTGAGGGCGCGCCAGGTGG 958
Db 497 ACGCGCTCAGCCACTGGGCGTGGCGCGAGGTGAGGTGTTGACGGGCTTCGGCTTGA 556
Qy 959 TGTGCTGTGACTGCAACCCCGCGCAGTCGGCGCTTCTGTGAGCTGAAGAAGTGTGCCATTC 1018
Db 557 AGGTGCCCCAGCCGAAGCCCGGAGTTCGGGCAACGCCCGCGCGAGCAGGTG---AAGG 613
Qy 1019 AGCAGCTGAGATTGAGACAGTGTGGCAGCTGTTCGGCGAGGGGTGCAACCGCGCATTC 1078
Db 614 TGCCTGTGGAGCGCCCGACCGCTGCCCGCGCTACGTGGCGCGCTGTGTGGAGAACGTGA 673
Qy 1079 AGGAGCTGTACGAGAAAGCTGGCGCCCTTCTGTGTGCAAAACAGCCACAACTTCTGGT 1138
Db 674 AGATTGGCGGTCTCCGAGTGTGATGAGACCGGTGAGGGCGCGCGGGGTGGCGGCA 733
Qy 1139 CCAAGCGCTCTGTACTTCCAGCAGCGCTGTACTACAGGGCGGATGGCAAGCTGT 1198
Db 734 TCAACAAGTGTGTGATGTACCAACTACGTGAACCTGGAGTACGGGACGCGCTGCACG 793
Qy 1199 GCTGGGTGTGCTGAGTGTGCGCTGTGTGGAGCTGTGGGCAAGACCGTCAAGCGCTCG 1258
Db 794 CTTTCGACCTGTGAGAAAGCTGGCGCGGTCAAGAGATTGTGCTCCGTACGGCGACGGCGCG 853
Qy 1259 CCAAGCGCCCAATAGGAGGACGCGCCCTGTGTGGGACAGCAACATGTCTATCCACT 1318
Db 854 AGAAGCTCAAGACCTGGAAGGCAAGNCCGCTTCCGTGGACGTGATGACCTGTGTATCG 913
Qy 1319 TCGTGAAGAACGGGCCCAAGCCGCTGTGTGTGGCTGTTCGTCAAGTTCTGTGAGCTGTG 1377
Db 914 CGGACAAAGGACCGGGCGCAGGCCCATCGTGTGCGTTCATGGGCGGCGGACACGAGGTG 972

RESULT 6
US-09-902-540-8514
; Sequence 8514, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16883
; PRIOR FILING DATE: 2000-07-10

Db 785 AAGAGGCGAGGAGCGCTCTTCTTCTGCTGAGGCGAGCGCGCTGCGCGAC 844
Qy 970 TGAACCCCGCGAGTGGCGCTTCTGAGCTGAAGAAGTGGCCATTACAGAGCTGGAG 1029
Db 845 CTGGACGACGTGGAGTGGAGCACCTGGAGCACCTGGCGCGAGTGGCGCGAAGCTGGCC 904
Qy 1030 TTGAGGAGCTGTGCACTGTTTGGCGAGGCGGTGCACCGCATTTGAGAGCTGTAC 1089
Db 905 ACGTACTGCTGGTGGAGTTGATGGAGCGGACGCGCTGCGCGCGCGCTGCGCGCTCC 964
Qy 1090 GAGAAGAGCTGGCGCCCTTCTGTGCG 1116
Db 965 CACCGGAGCGAGCGGAGCGTGTGCG 991

RESULT 9

US-09-881-165-4
; Sequence 4, Application US/09881165
; Patent No. 6632930
; GENERAL INFORMATION:
; APPLICANT: HOOD, ELIZABETH
; APPLICANT: HOWARD, JOHN
; APPLICANT: BAILEY, MICHELE
; APPLICANT: GASTEL, FRANS VAN
; APPLICANT: WANG, HUAMING
; APPLICANT: WARD, MICHAEL
; APPLICANT: WOODARD, SUSAN
; TITLE OF INVENTION: METHOD OF INCREASING RECOVERY OF HETEROLOGOUS ACTIVE
; FILE REFERENCE: 10032R
; CURRENT APPLICATION NUMBER: US/09/881,165
; CURRENT FILING DATE: 2001-08-14
; PRIOR APPLICATION NUMBER: 60/211,732
; PRIOR FILING DATE: 2000-06-15
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 4
; LENGTH: 1082
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA encoding
; OTHER INFORMATION: Organophosphate Hydrolase
US-09-881-165-4

Query Match 3.2%; Score 62.4; DB 3; Length 1082;
Best Local Similarity 44.6%; Pred. No. 0.003;
Matches 246; Conservative 0; Mismatches 306; Indels 0; Gaps 0;
Qy 1371 CTTGTGCTCTTCAACAGGCGGTGCTGTGTTGGCGGGCGGTGCGCGGCAAGCAGTA 1430
Db 515 CCAGAGCTGCTGTCTCAAGGCGCGCGCGCGCTCTCCGCCACCGCGGTGAC 574
Qy 1431 CGCGTGTATCAAGCGGAGCGGATCCCATTTGAGAACTACATCGCGCGCACCATGGACGG 1490
Db 575 CACCCACACCGCGCTCCAGCGGAGAGCGGAGCAGCAGCGCGCATCTTCGAGTCCGA 634
Qy 1491 CGTGGCGGAGAACTCGCACGTGCGCAAGCAGAACTACTTCTACTACAACTGCCTCACCGG 1550
Db 635 GGGCTCTCCCGTCCCGGTGTGATCGGCGACTCCGACGACACCGACGACCTCTCTA 694
Qy 1551 CAAGTTCTGCGGAGCAACTGCCCCCACTTACCTGGCGAGGGCGGCTTCGCGACCTCAA 1610
Db 695 CTTACCGCCCTCGCGCGCGCGGTACTCTCATCGGCTCGACCAATCCGCGCATCCGC 754
Qy 1611 GAGTGGCTGTGGACAACCTGACCGTCTCCACCAACTTCTTCATGGAGGAGCTCAAGC 1670
Db 755 CATCGGCTCGAGGACAACGCTCCGCTCGCCCTCTCGGCATCCGCTCTGCGAGAC 814
Qy 1671 GCGCACTTACCAAGGTGATTTGATGAGCAACGTTGAGTGGTGGATATGCCCGTGGC 1730
Db 815 CCGCGCCCTCTCTCATCAAGGCGCTCATCGACACAGGCTACATGAAGCAGATCCTCGTGC 874

Qy 1731 CAACGAGCTGCGCGAGTGCCTGGCCAAGCAGGTTGCGCGCGCGCATCGTCATCTGCGC 1790
Db 875 CAACGAGTGGCTTCTTGGCTTCTCTCTAGCTGAACCAACATCATGACGATGATGGACCG 934
Qy 1791 CTCGCGCTCTCCAGCCCGCGCTACGCGGAGCTGATCCAGAAAGCGGGCTTCGACGTGCG 1850
Db 935 CGTGAACCCGAGCGCATGGCTTTCATCCCGCTCCGCGTATCCGTTCTCCGCGAGAA 994
Qy 1851 CTGATCGCGCGCGCACTCAGGCTTACATGGACCGGTCAACATGTACAGTCTCTTTCTA 1910
Db 995 GGGCGTGGCGAGGAGACCTTCGCGCGCATCCGTCGACCAACCGCGCGCTTCTCTCTC 1054
Qy 1911 CATGCCCGCGC 1922
Db 1055 CCCGACCTCCG 1066

RESULT 10

US-09-902-540-2993
; Sequence 2993, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 2993
; LENGTH: 1167
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-902-540-2993

Query Match 3.2%; Score 62.4; DB 3; Length 1167;

Best Local Similarity 43.7%; Pred. No. 0.003;

Matches 340; Conservative 0; Mismatches 426; Indels 12; Gaps 1;

Qy 762 CGTTGGCCACGCTGTACGAGGAGCGGTGGAGCGCGCCCATGTTCCGCGCCACCTT 821
Db 351 CTTGAGCTACGCGCGCGGACGAGTTCGGTTCAGGTGACCCGCTGTCATGCGTACCT 410
Qy 822 CTTGTACACGCGAGTGTGGGAGGACCCGAGCCGGATATGAGGTGATGGAGATCAACCC 881
Db 411 GCGCGCCAGCATGCGGCGGAGCAGCGGAGCTGTGCGAGCACCTGAAGATCATCCAGGA 470
Qy 882 CAAGGACACGCTGTGACCCCTGACTAGCGGCGGTGCAATGCCCTGAACCTGTGTTGCA 941
Db 471 CGACATCAGGTACATCACCCTGGCCAGCGCTGAAGGCTGACCTCAACGTCGCGCGCT 530
Qy 942 GGGGGCGCGCAGGTGTGTGCTGGTGTGACTGCAACCCCGCGAGTCGGGCTTCTGGAGCT 1001
Db 531 GGCCTGGCGCTGGAGGCGCGCTCGGCTTCGACTTCAGCCACGTCAGCAAGGTGGAGCC 590
Qy 1002 GAAGAAAGTGGCCATTACGACAGCTGGAGTTTGGAGAGCTGTGGCA-----GCT 1049
Db 591 GGAGGCTTCCGAAGCTGGAGCAGGTGTGAGACGCGGCGGCGGCGGCGCAGCTGGT 650
Qy 1050 GTTCGGCGAGGCGTGCACCCCGCATTTGAGAGCTGTACAGAAAGCTGTGGCGCCCTT 1109
Db 651 GTTGTGCGGCTGTGCGCGCGCGCTTGGCGGTGCTGCGCGCTCGGCGCAAGGTTTGC 710
Qy 1110 CTTGTGCAAAACCGACACAACTTCTGTTCAAGGCTCTGTGACTTCCAGACGCGCT 1169
Db 711 GGTGCGGCTGGCCACGCTGTGGCTGCGCTGTGATGTCGCCAACTGCGGCGGAGTGAGCA 770
Qy 1170 GTACTACAGGCGGCGCATGGGCAAGCTGTGTGGGTGTGTCAGTGCCTTGGCGCTGCT 1229

Accession	Sequence	Length
771	CCAGGGCTTCAAGCGCGGAACTACTGGCCAGGCTGGGGCGAGCGCTCCGGCGTGGG	830
1230	GGGACTGGGCAAGACCGTCAAGCGCCTTGGCAACCGCCCACTATGGAGGACAGCGCCG	1289
831	GGTGCGGTGCCCATCTTCGGCGGCAAGCGCGCGTCCCCCACATGCCCAGCTCCAGGG	890
1290	TCGTGGGACAGCAACATGCTCATCTCACTTGTGAAGAAAGGGGCCCAAGCGCTGTGTG	1349
891	GCTCTTGGCGCGGTGCACTGACGAGACCGGCGCTGGAGACCTGGAGCGCTGGAGAC	950
1350	GCTCTTCGTCAAGTTCGTGAGCCTGTGTCTTCAACAAGCGCTGTGTGTTCGGCGG	1409
951	TCGGCGCCTCAGTCAGTACTCTTCGGGGCCACGAACATCGACCCGGCGCGCTCAGGG	1010
1410	CGGCGTGC CGGCGAAGCAGTAGTACGCGCTGATCAAGCGGACGGCATCCCCATTGAGAACTA	1469
1011	CGGTCCACGGACATCTCCAACCTCGCTGGGAGCACCAGCTGAACATCATCCGCGGCT	1070
1470	CATCGCGGCACATGACGCGGTGGCGGAGAACTCGCATCGTGGCAAGCAGAACTAC	1527
1071	GGGACAGGGGGCATGGCGGAGGTCTTCCTCGCCCAAGCAGGTGGCGCTGAAGGCTTC	1128

RESULT 11

```

US-09-902-540-362
; Sequence 362, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 362
; LENGTH: 1250
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-902-540-362

```

Query Match	3.2%;	Score 62.4;	DB 3;	Length 1250;
Best Local Similarity	43.7%;	Pred. No. 0.003;		
Matches 340;	Conservative 0;	Mismatches 426;	Indels 12;	Gaps 1;
QY	762	CGTTGGCCACGCCTGCACGAGGAGCGGTGGAGCGCGCCCATGTCTTCGCCGCCACCTT	821	
DB	434	CTTCGACTACGCGGGCGGACAGTTTCGGTCAAGTGGACCCGGTGGTATGCGCTACCT	493	
QY	822	CCTGTACACGCAGTCGTGGGAGGACCCCGAGCCGGATATGAGGTGATGAGATCAACCC	881	
DB	494	GCSCGCCAGCATGCCSCGCGAGCAGCGGAGCTGTCGCASCACCTGAAGATCATCCAGGA	553	
QY	882	CAAGGACACGGTGTGACCTGTAGCTAGCGCGCGGTGCATGCCCTGAACCTGTGTGTGCA	941	
DB	554	CGACATCACGTACATCACCCCTGGCCACGCGCGCTGAAGGGTGACCTCAACGTGCGCGGCT	613	
QY	942	GGGGGCGGCGCAGTGTGTTCGTGGACTGCAACCCCGCGCAGTCGCGCGCTTCTGAGACT	1001	
DB	614	GGGCTCGGGCTTGAGGGCGCGTTCGGCTTCGACTTCAGCCAGCTCAGCAGGTGGAGCC	673	
QY	1002	GAAGAAAGGTGGCCATTGAGCAGCTGGAGTTTGAGGACGTGTGGCA-----GCT	1049	
DB	674	GGAGGCCCTCCGAAAGCTGTGAGCAGGTGCTGGAGACGGCGCGCAGGCGCGCACGTGGT	733	
QY	1050	GTTCCGGGAGGGCGTGCACCCCGGCATTGAGGAGCTGTACGAGAAAGCTGCGGCCCTT	1109	
DB	734	GTGTGTCGGGTGCGCGCGTGGCGGTGGCGGTGCTGGCGCGCTCGGCCAAGGTGTGCG	793	

Qy	1110	CTGTGCGCAACGAGCCACAACTTCTGGTCCAAAGCGCCTCTGTACTTCCAGCAGCGCCT	1169
Db	794	GGTGCGCTGCGCCACAGCTGTGGCTGCGGTGACTGCGCAACTGCGGGCAGGTGAGCCA	853
Qy	1170	GTACTACAGGCGGGCATGGCAAGCTGTGCTGGGTCTGTCAGTGCCTGCGCCCTGTGCT	1229
Db	854	CCAGCGCTTCCAAAGCCGGGACTACTTGGCAGGCTGCGGGCGAGGCGTCCCGCGTGGGA	913
Qy	1230	GGGACTGGGCAAGACCGTCAAAGCGCCTCGCCAAACGGCGCCCACTAATGAGGAGCAGCGCCG	1289
Db	914	GGTGCGTGGCCCATCTGTCGGCGGCAACGCGCGGTCCCCCATGCCCCAGCTCCAGG	973
Qy	1290	TCTGTGGGACAGCAACATGCTCATTCACATTCGTGAAGAACGGGCCCAAGCCGCTGTGTG	1349
Db	974	GCTGCTGGCGGGGTGCAGTGCAGGACCGGCCGCTGGAGGACTCTGAGGCGCTGGAGAC	1033
Qy	1350	GCTGTTGCTCAAGTTCGTGAGCCTGTGTGCTCTTCAACAGGCGCTGCTGTGGTTCGGCGG	1409
Db	1034	TGCGGCCCTCAGTCACTGATCCTCTTCGGGCGCCAGAACATCGACCCGCGGCCGTCAGGG	1093
Qy	1410	CGGCGTCCGGGCAAGCAGTACGCGCTGTATCAAAGGCGGACGGCATCCCCATTGAGAACTA	1469
Db	1094	CGGCTCAGCGACATCTCCAACTCGTGGGACGACCAAGCTGAACATCATCCGCGGCT	1153
Qy	1470	CATCGGCGGCACCATGGAACGCGCTGGGGNGAACTCGCACGTCGCGGACGAGAACTAC	1527
Db	1154	GGGACAGGCGGATGGCGAGGTCTTCCTCGGCAAGCAGGTGGGCGTGAAGGCTTC	1211

RESULT 12

```

US-09-902-540-7318
; Sequence 7318, Application US/09902540
; Patent No. 6833447
;
; GENERAL INFORMATION:
;
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
;
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
;
; FILE REFERENCE: 38-10(15849)B
;
; CURRENT APPLICATION NUMBER: US/09/902,540
;
; CURRENT FILING DATE: 2001-07-10
;
; PRIOR APPLICATION NUMBER: 60/217,883
;
; PRIOR FILING DATE: 2000-07-10
;
; NUMBER OF SEQ ID NOS: 16825
;
; SEQ ID NO 7318
;
; LENGTH: 3579
;
; TYPE: DNA
;
; ORGANISM: Myxococcus xanthus
US-09-902-540-7318

```

	Query Match	3.2%	Score 62.2	DB 3	Length 3579	
	Best Local Similarity	42.3%	Pred. No. 0.0039			
	Matches 474	Conservative	0	Mismatches 638	Indels 9	Gaps 2
Qy	821	TCCTGTACACGCACTCGTGGAGGACCCCGAGCCGGATATGAGAGGTGATGGAGATCAAC	880			
Db	1517	TCCAGGACGCAAGTGTCTGGAGGCCAAGACACAAAGGCAACGCCGGGCAAGC	1576			
Qy	881	CAAAGGACACGGTGTGACCCCTGACTAGCCGGCTGCAATGCCCTGMAACCTGCTGGTGC	940			
Db	1577	CGGGCAAGTGGCTGCAAGAACGCCCTACTAACCGGTGTGGCTTACGACGAGGTGCTCA	1636			
Qy	941	AGGGGGCCGCCAGGTGGTGTCTGGTGGACTGCAACCCCGCAGTCCGGCGCTTCTCGAGC	1000			
Db	1637	AGCGGGCGAGGCGCGGGGCGAGGGCAAGACGAGCGGTGGCTCGGACATCACCAAGA	1696			
Qy	1001	TGAAGAAGTGGCCATTACAGACCTCGAGTTTGAGACAGTGTGGCAGCTGTTCCGGCAGG	1060			
Db	1697	AGGCCACCACTCCCAACGCTGAAGAAGCGCGTGTCAACCGGTGTGACGCGTACTCAAGT	1756			
Qy	1061	GCGTGCAACCCGCGCATTTGAGGAGCTGTACAGAGAAGAGCTGGCGCCCTTCTCTGCGCAA	1120			

||||| ACCTGCCAAGGGTGAAGCGGGTGGAGATCGCTTCAAGCGCGCCAAACATCTACTACC 1816
Db
||||| CCAGCCCAAACTTCTGGTCCAAAGCGCTCTGGTATCTTCCAGCAGCGCTGTACTACGAG 1180
Qy
||||| GCCACAACCACTTCCAGAGCGGGTGGCTTTCAGCGAGATCGCGCTCGGCTACCCCG 1876
Db
||||| CGGCAATGGGCAAGCTGTGTGGGTGTCTGACGTGCTGCGCGGTGGTGTGGGATCGGGCA 1240
Qy
||||| AGTACAAAGTTTCAGAACGGCGAGCGCGGGGGAGATCTCCGCCAACTCATCTCGACT 1936
Db
||||| AGACCGTCAAGCGCTCGCCAAACCGCCCAAAATGGAGGAGCAGCGCGCTGTGGGACA 1300
Qy
||||| GTTACCACCTCTGACGACTTACCGAAGGTGAACGAGTGGCGGGCGCTTCTACGCCA 1996
Db
||||| GCAACATGC-----TCATCACTTCTGTGAAGAACGGGCCCAAGCGCTGTGTGGTGT 1354
Qy
||||| ATGCAAGCTGGCGTGGGCAAGTTCCGCGACGACCTTGGCGAAGTCTCATCGACGATCGT 2056
Db
||||| TCGTCAAGTTCTGTGAGCTGTCTTCAACAGGCGGTGCTGTGTTCGGCGCGCG 1414
Qy
||||| CTTTCAAGCTCTGACGAGCTTGGAGGAGAAAGAGTTTCGAAAGGCCCGCGAGGCGT 2116
Db
||||| TCGCGGGCAAGCAGTACGCGCTGATCAAGGCGGACGCGCATCCCATTTGAGAACTACATCG 1474
Qy
||||| ACTTCGCTTCTGTAAGACTTCCGCGAGACGGAGATCGCGACTTGGCGCTTACAACG 2176
Db
||||| CGCGCAACATGAGCGGCTGGCGGAGAACTCGACGTGGCGGCAAGAGAACTTCTTACT 1534
Qy
||||| CGTCCGTCTGACTTACAAGCGAAGCGCTGGATTAAGGCCATCGAGGTGCGCAAGCGCC 2236
Db
||||| ACAACTGCTCACCGGCAAGTTCTGGCGGACAACTGCGCCCACTACCTGCGCGAGGG 1594
Qy
||||| TGGTTCGCGAGTAACCGGCTTCCAAAGCACGTGCGGACTCCATCTACCGCAACGCGAGG 2236
Db
||||| CTTTTCGCCCACTCAAGAGTGGCGTGGTGAACAACTTACCGCTTCCACCAACTTCTTCA 1654
Qy
||||| CGCTGGAGGCAATTTGGCGACTTTCAGGAGCGCGCGCAACGTAACGAGGCTTACGTGCGG 2356
Db
||||| TGGAGGAGCTCAAGCGCGCACTTACACCAAGGTGATTTCTATGAGCAACGTGAGTGGC 1714
Qy
||||| GCTACGAGCGAGCTGGTGTGACAAAGGGCAACGCAAGCGCGTGTGGCGGCAAGAGA 2416
Db
||||| TGGATATCGCGTGGCAACAGCTGGCGGAGTGGTGGCGCAAGCGTTCGCGC--GG 1771
Qy
||||| AGCGGGCGCGGTGACACAAACAAAGCCCGGTGGTGCAGAAAGTGGAGCGAGTCCAAAG 2476
Db
||||| CGCGCATCGTTCATCTGGCGCTCCGCTTCCCTCAGCCCGCCCTACGCGAGCTGATCCAGA 1831
Qy
||||| CGCAGTGGCGCTCTTCAACCGCGCCACTACCGAGAGGGCTTGGCGCAGTGAAGCGG 2536
Db
||||| AGCGGGCTTCGAGTGGCGTGCATCCCGCGGCACTCAGGGGTCTATGAGACCGGTCA 1891
Qy
||||| CGCTGCGCAACCGCGAGCACTACCTGACGTGTGGCGCGCGCAAGGACGCGCACGAA 2596
Db
||||| ACATGTACAGTCTCTTACATGCGCCCGCGGAAGGGCGCC 1932
Qy
||||| TCCGCTCTCCATCATCACTGACGCGCAAGAGCGCGGCC 2637
Db

RESULT 13

US-09-902-540-694
; Sequence 694, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10

; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 694
; LENGTH: 5656
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
; US-09-902-540-694

Query Match

Best Local Similarity 3.2%; Score 62.2; DB 3; Length 5656;
Matches 474; Conservative 42.3%; Pred. No. 0.0042;
Matches 474; Mismatches 638; Indels 9; Gaps 2;

Qy 821 TCCTGTACAGCAGTCTGTGGGAGACCCCGAGCCGGATATGGAGTGTATGAGATCAAC 880
Db 3573 TCCAGGACGCCAAGTGTCTGGAGCCAGAGACAGAGGCAAGCCGAGCGGCAAGC 3632
Qy 881 CCAAGGACACGGTCTGACCCCTGACTAGCGCGGCTGCAATGCCCTGAACTCTGTGTGC 940
Db 3633 CGGCAAGTGGCTGCAGAACCGCCCTACAAACGCGGTCTGGCTTACGACGAGTCTCA 3692
Qy 941 AGGGGCGGCGCAGGTGTCTGCTGAGTGTGCACTGCAACCCCGCGCAGTCCGGCGTTC 1000
Db 3693 AGCGGCGGCGAGCGCGCGGCGAGGCAAGAGCGAGCGGTGGCTCGGACATCAACA 3752
Qy 1001 TGAAGAAAGTGGCCCATTTACGACGCTGGAGTTTGAAGAGCTGTGCGAGCTGTCG 1060
Db 3753 AGGCCACATCCCTCCACGCTGAAGAGGCGTCTGCGACGCTGTGAGGCGTCTCAAG 3812
Qy 1061 GCGTGCACCGCGCATTTGAGAGAGCTGTAACGAAAGAGTGGCGCGCTTCTGTGCGAAA 1120
Db 3813 ACGTGCACCAAGGTGAGAAAGCGGTGGAGATCGCTTCAAGGCGGCGCAACATCTACT 3872
Qy 1121 CCAGCCAACTTCTGTGCTCAAGCGCTCTGGTACTTCCAGCAAGGCTGTACTACGAG 1180
Db 3873 GCCAACCACTTCTGAGCGCGGTGTGCGCTTTCAGCGAGATCGCGCTCGGCTACCC 3932
Qy 1181 CGCGCATGGGCAAGCTGTGTGGGTGTGCAAGTCTGCGCGCTGTGCTGGAGTGGGCA 1240
Db 3933 AGTACAAAGTTTCAGAAACCGCGAGCGCGCGGAGATCTCGCCNAACCTCATCTCTCA 3992
Qy 1241 AGACCGTCAAGCGCTCCCAACCGCCCAAAATGGAGGAGCAGCGCGCTGTGGGACA 1300
Db 3993 CGTACCACTCTCTGACGAGTACCGAAGGTGAACGAGTGGCGCGCGCTTCTACGCCA 4052
Qy 1301 GCAACATGC-----TCATCCACTTCTGAGAAAGGGGCCCAAGCGCTGTGTGCTGT 1354
Db 4053 ATGACAAAGTGGCGGTGGGCAAGTTCCGCGACGACCTTGGCGAAGCTCATCGAGCAT 4112
Qy 1355 TCGTCAAGTTCTGAGCTGTGTGCTCTTCAACAAAGGCGCTGTGTGTTCGGCGCGCGG 1414
Db 4113 CTTTCAAGTCTGTGACGAGTTCGAGGAGAGAGAGGATTCGAGAAAGCCCGGAGGCG 4172
Qy 1415 TGGCGGCAAGCAGTACGCGTGTATCAAGGCGGACGGCATCCCCATTGAGAACTATAC 1474
Db 4173 ACCTCGCTTCGTGAAGGACTTCCGCGAGACGAGATCGCGGACCTGCGCTCTACAAC 4232
Qy 1475 CGCGCAACATGGACGGCGTGGCGGAGAACTCGCAGCTGCGCAAGCAGAACTTCTTACT 1534
Db 4233 CGTCCGCTGACTACTACAAGCGCAAGCGCTGGATAAGGCCATTCGAGTGGCGAAGCGCC 4292
Qy 1535 ACAACTGCTCACCGGCAAGTTCTTGGCGGACAACTGCCCCACCTTACCTGCGCGAGGCGG 1594
Db 4293 TGGTTCGCGAGTACCGCGCTCCAAAGCACGCTGCCGACTCCATCTACGCAAGCGGAGG 4352
Qy 1595 CTTTCCGCCAACCTCAAGAGTGGCGGTGGTGGAGCAACCTGTACCGCTTCCACCAACTTCT 1654
Db 4353 CGCTGGAGGCGCATTTGGCGACTTTCGAGGACGCGGCGGCAACGTAACGAGGCTTACGT 4412
Qy 1655 TGGAGGAGCTCAAGCGCGCACCTTACACAGGTGATTTCTGATGAGACCACTGAGTCTGC 1714
Db 4413 GCTACGAGCGCAGCTGGGTGACAAGGCAACGCGCGCGGTGGTGGCGGCAAGAGA 4472

QY 1715 TGGATATGCCGTGGCCAAAGAGCTGGCGGAGTGGCTGGCCAAAGCAGGTTCGGCC---GG 1771
Db 4473 AGCGGGGCGGTGGAGACAAAGACCGCGGTGGTGCAGAAAGTGGGACGAGTCCAAAGG 4532
QY 1772 GCGGCATCGTATCTGGCGCTCCGCTCCCTCAGCCCGCTTACCGCGAGCTGATCCAGA 1831
Db 4533 CGAGTGGCGCTCTTCAACGCGGCACCTACCGAGAGGCTTGGGCCAGGTGAAGGCGG 4592
QY 1832 AGCGGGTTCAGCTGGCTGCATCCGCGCGCCACTCAGGGCTTACATGGACCGCGTCA 1891
Db 4593 CGCTGCGAAACGCGAGCACTACCTGACGCTGTGGCCGCGCGAAGGACGCGCAGAA 4652
QY 1892 ACATGTACAGCTCTTCTACATGGCCGCGCGGAAGGGCGCC 1932
Db 4653 TCCGCTCTCCATCATCGACCTGACGGCGCAAGAGCGGCGCC 4693

RESULT 14

US-09-902-540-6237
; Sequence 6237, Application US/09902540
; Patent No. 6833447

; GENERAL INFORMATION:

; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 6237
; LENGTH: 981
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-902-540-6237

Query Match 3.2%; Score 61.8; DB 3; Length 981;

Best Local Similarity 49.8%; Pred. No. 0.0038;

Matches 156; Conservative 0; Mismatches 157; Indels 0; Gaps 0;

QY 1443 GCGGACGGCATCCCATTTGAGAACTACATCGCGCACCATGAGACGGCGTGGCGGAGAA 1502
Db 246 GGACGGCAGCGGTACCTCAATCACTCATCTGTGTGCGCAAGGCGCGCGCGCGAGCC 305
QY 1503 CTCGACGTGCGCAGCAGAACTACTTCTACTACAACTGCCTCACCGCAAGTTCTTGGC 1562
Db 306 CCCGAGACGTTGAAGACGGAACCCGCTGTGTACCAAGGCGGCTCCGGGGACTTCTTGGC 365
QY 1563 GGACAACTGCCCCACTTACTTGGCGAGGCGGCGCTTCCGCCACCTCAAGAGTGGCGTGGT 1622
Db 366 GCCACCGCGACATCCCTCTGGCGAGCAGAGCTTGGGGCTTGGATTCGAAGGCGAGGT 425
QY 1623 GGACAACTGACCGCTCTCCACCAACTTCTTATGAGGAGTCAAGCGCGCACCTACAC 1682
Db 426 CTGGCCATCTTGGCGGACACGCCCGGACGAGGCGGAGAACGCGCGCGCGCAGT 485
QY 1683 CAAGGTGATTCGTATGGACACGAGTGGATGGCTGGATATGCCGTGGCCAAAGCTGGC 1742
Db 486 CAAGCTGTGTATGCTGGCCAAATGACGTGTCTTGGCAACCTCATCCCAACGAGCTGGC 545
QY 1743 CGAGTGGCTGGCC 1755
Db 546 CAAGGGCTTCGAC 558

RESULT 15

US-09-902-540-1047

; Sequence 1047, Application US/09902540

; Patent No. 6833447

; GENERAL INFORMATION:

; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 1047
; LENGTH: 13332
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-902-540-1047

Query Match 3.2%; Score 61.8; DB 3; Length 13332;

Best Local Similarity 49.8%; Pred. No. 0.0058;

Matches 156; Conservative 0; Mismatches 157; Indels 0; Gaps 0;

QY 1443 GCGGACGGCATCCCATTTGAGAACTACATCGCGCACCATGAGACGGCGTGGCGGAGAA 1502
Db 11288 GGACGGCAGCGGTACCTCAATCACTCATCTGTGTGCGCAAGGCGCGCGCGCGAGCC 11347
QY 1503 CTCGACGTGCGCAGCAGAACTACTTCTACTACAACTGCCTCACCGCAAGTTCTTGGC 1562
Db 11348 CCCGAGACGTTGAAGACGGAACCCGCTGTGTACCAAGGCGGCTCCGGGACTTCTTGGC 11407
QY 1563 CGACAACTGCCCGACCTACCTGCGGAGGCGGCGCTTCCGACCCCTCAAGAGTGGCGTGGT 1622
Db 11408 GCCACCGCGACATCCCTTGGCGGACGAGGCTTGGGGCTTGGATTCGAAGGCGAGGT 11467
QY 1623 GGACAACTGACCGCTCTCCACCAACTTCTTATGAGGAGTCAAGCGCGCACCTACAC 1682
Db 11468 CTGGCCATCTTGGCGGACACGCCCGGACGAGGACGAGGCGGCGCGCGCAGT 11527
QY 1683 CAAGGTGATTCGTATGGACACGCTGGAGTGGCTGGATATGCCGTGGCCAAAGCTGGC 1742
Db 11528 CAAGCTGTGTATGCTGGCCAAATGACGTGTCTTGGCAACCTCATCCCAACGAGCTGGC 11587
QY 1743 CGAGTGGCTGGCC 1755
Db 11588 CAAGGGCTTCGAC 11600

Search completed: May 4, 2006, 18:51:27

Job time : 368 secs

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GenCore version 5.1.1.7
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 4, 2006, 19:00:04 ; Search time 953 Seconds
(without alignments)
8320.283 Million cell updates/sec

Title: US-10-620-914-44

Perfect score: 1947
Sequence: 1 atgggggtcggtcgtagcgg.....gcgcgaagaagacaactaa 1947

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 9306428 seqs, 2036268586 residues

Total number of hits satisfying chosen parameters: 18612856

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database :
- 1: /SID85/ptodata/2/pubpna/US08_NEW_PUB.seq1.*
 - 2: /SID85/ptodata/2/pubpna/US06_NEW_PUB.seq.*
 - 3: /SID85/ptodata/2/pubpna/US07_NEW_PUB.seq.*
 - 4: /SID85/ptodata/2/pubpna/US08_NEW_PUB.seq.*
 - 5: /SID85/ptodata/2/pubpna/PCT_NEW_PUB.seq.*
 - 6: /SID85/ptodata/2/pubpna/US09_NEW_PUB.seq.*
 - 7: /SID85/ptodata/2/pubpna/US09_NEW_PUB.seq1.*
 - 8: /SID85/ptodata/2/pubpna/US09_NEW_PUB.seq2.*
 - 9: /SID85/ptodata/2/pubpna/US10_NEW_PUB.seq.*
 - 10: /SID85/ptodata/2/pubpna/US10_NEW_PUB.seq1.*
 - 11: /SID85/ptodata/2/pubpna/US10_NEW_PUB.seq2.*
 - 12: /SID85/ptodata/2/pubpna/US10_NEW_PUB.seq3.*
 - 13: /SID85/ptodata/2/pubpna/US10_NEW_PUB.seq4.*
 - 14: /SID85/ptodata/2/pubpna/US11_NEW_PUB.seq.*
 - 15: /SID85/ptodata/2/pubpna/US11_NEW_PUB.seq2.*
 - 16: /SID85/ptodata/2/pubpna/US11_NEW_PUB.seq3.*
 - 17: /SID85/ptodata/2/pubpna/US11_NEW_PUB.seq4.*
 - 18: /SID85/ptodata/2/pubpna/US11_NEW_PUB.seq5.*
 - 19: /SID85/ptodata/2/pubpna/US60_NEW_PUB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	66	3.4	1577	US-11-096-568A-10906	Sequence 10906, A
2	64	3.3	2736	US-10-858-730-38	Sequence 38, Appl
3	62	3.2	4770	US-10-496-351-3	Sequence 3, Appl
4	62	3.2	82746	US-10-496-351-56	Sequence 56, Appl
5	61.2	3.1	4773	US-11-100-356-55	Sequence 55, Appl
6	61.2	3.1	5283	US-11-100-356-54	Sequence 54, Appl
7	60.8	3.1	1325	US-11-096-568A-1077	Sequence 1077, Ap
8	59.6	3.1	1347	US-11-096-568A-12531	Sequence 12531, A
9	59.6	3.1	2799	US-11-100-356-53	Sequence 53, Appl
10	57.8	3.0	1599	US-11-096-568A-26187	Sequence 26187, A
11	57.6	3.0	1444	US-11-096-568A-20988	Sequence 20988, A
12	57.2	2.9	1906	US-11-166-609-1	Sequence 1, Appl
13	56.2	2.9	3513	US-10-858-730-142	Sequence 142, App
14	56	2.9	4282	US-11-183-624-1	Sequence 1, Appl

15	56	2.9	4282	17	US-11-183-624-3	Sequence 3, Appl
16	55.2	2.8	1243	18	US-11-096-568A-25531	Sequence 25531, A
17	55.2	2.8	88421	17	US-11-205-109-1	Sequence 1, Appl
18	55	2.8	14055	13	US-10-496-351-1	Sequence 1, Appl
19	54.8	2.8	88421	17	US-11-205-109-1	Sequence 1, Appl
20	54.6	2.8	1283	18	US-11-096-568A-23551	Sequence 23551, A
21	54.4	2.8	2472	18	US-11-100-356-32	Sequence 32, Appl
22	54	2.8	2025	17	US-11-167-048-2	Sequence 2, Appl
23	53.8	2.8	2403	11	US-10-649-457-4	Sequence 4, Appl
24	53.8	2.8	3639	18	US-11-100-356-33	Sequence 33, Appl
25	53.8	2.8	37507	10	US-10-522-037-2	Sequence 2, Appl
26	53.6	2.8	1182	18	US-11-096-568A-26293	Sequence 26293, A
27	53.6	2.8	1580	18	US-11-096-568A-20206	Sequence 20206, A
28	53.6	2.8	2466	18	US-11-100-356-31	Sequence 31, Appl
29	53.6	2.8	2873	17	US-11-136-527-2776	Sequence 2776, Ap
30	53	2.7	1292	18	US-11-096-568A-19003	Sequence 19003, A
31	52.8	2.7	1958	18	US-11-096-568A-26982	Sequence 26982, A
32	52.8	2.7	3387	17	US-11-091-883-183	Sequence 183, App
33	52.8	2.7	3439	17	US-11-000-888-851	Sequence 851, App
34	52.6	2.7	1572	18	US-11-096-568A-19140	Sequence 19140, A
35	52.6	2.7	1971	18	US-11-100-356-38	Sequence 38, Appl
36	52.2	2.7	645	13	US-10-496-351-6	Sequence 6, Appl
37	52.2	2.7	1672	13	US-10-943-508A-16	Sequence 16, Appl
38	52.2	2.7	1859	18	US-11-096-568A-25607	Sequence 25607, A
39	52.2	2.7	30191	11	US-10-330-773-631	Sequence 631, App
40	52	2.7	1401	18	US-11-096-568A-22550	Sequence 22550, A
41	52	2.7	3624	11	US-10-755-092-6	Sequence 6, Appl
42	51.6	2.7	2007	18	US-11-100-356-61	Sequence 61, Appl
43	51.6	2.7	2007	18	US-11-100-356-62	Sequence 62, Appl
44	51.6	2.7	2007	18	US-11-100-356-63	Sequence 63, Appl
45	51.6	2.7	2028	18	US-11-100-356-19	Sequence 19, Appl

ALIGNMENTS

RESULT 1

US-11-096-568A-10906
; Sequence 10906, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nickolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides I
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096.568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 10906
; LENGTH: 1577
; TYPE: DNA
; ORGANISM: Triticum aestivum
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(1577)
; OTHER INFORMATION: Ceres Seq. ID no. 13597454
US-11-096-568A-10906

Query Match 3.4%; Score 66; DB 18; Length 1577;

Best Local Similarity 47.2%; Pred No. 1.4e-06;
Matches 201; Conservative 0; Mismatches 225; Indels 0; Gaps 0;

Qy	1408	GGCGCGTGGCGGCAAGCAGTACGCGTGTATCAAGCGGCGGCGCATCCCCATTGAGAAC	1467
Db	315	GGATACATCGCGGCGCGCTCTACGACCTGACGCGTCCAAGTACGGCACGCGGTGGAG	374
Qy	1468	TACATCGGCGCACCATGAGCGGTGGCGGAGAACTCGGACGTGCGCAAGCAGACTAC	1527
Db	375	CTCAGTGTCTCATCGGCGCTTCGTCGCCAAGGCGCATCAAGTGTGCGCGCATCGTC	434
Qy	1528	TTCTACTACAACTGCTCACCGGCAAGTTCCTGCGCGCAACTGCCACCTACCTCGCGC	1587
Db	435	ATCAACCAACCGCTGCGCGGAGGACAAGACGGGCGGCGCATCTACTGTCTTCAAGGCG	494

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QY 1588 GAGCGGCTTCGCCACCCCTCAAGAGTGGCGTGGGACAACTGACCGTCTCCACCAAC 1647
Db 495 GGAGGACCCGAGGGCTCTCTGGACTGGGGTCCGGGCATGATCTCGAGCGCAGACACCAAG 554
QY 1648 TTCTTCATGGAGAGCTCAAAAGCGGCACCTACACCAAGGTGATTCTGATGGACCACTG 1707
Db 555 TTCTCCGACGGACGGGTACCGTGATACCGGCGGGACTTCGGCGCGCGCCGACATC 614
QY 1708 GACTGGCTGGATATGCCCGTGGCCAAAGAGTGGCCGAGTGCCTGGGCCAAGAGTTGCG 1767
Db 615 GACCACCTCAACCCGCGGTCAGAAAGAGTCTCCGACTGGCTCAAATGGCTCAAGTCC 674
QY 1768 CGGGCGGCATCGTATCTGGGGTCCGCTCCCTCAGCCCGCCCTAGCGCGAGTGTATC 1827
Db 675 GACCTCGGCTTCGACGGCTGGCGCTCGACTTCGCCAAGGGCTACTCGGCGGAGCTGCC 734
QY 1828 CAGAAG 1833
Db 735 AGGACG 740

RESULT 2
US-10-858-730-38
; Sequence 38, Application US/10858730
; Publication No. US2005025568A1
; GENERAL INFORMATION:
; APPLICANT: Bailey, Richard B.
; APPLICANT: Blomquist, Paul
; APPLICANT: Doten, Reed
; APPLICANT: Driggers, Edward M.
; APPLICANT: Madden, Kevin T.
; APPLICANT: O'Leary, Jessica
; APPLICANT: O'Toole, George
; APPLICANT: Trueheart, Joshua
; APPLICANT: Walbridge, Michael J.
; APPLICANT: Yorgey, Peter S.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR AMINO ACID
; TITLE OF INVENTION: PRODUCTION
; FILE REFERENCE: 14184-030001
; CURRENT APPLICATION NUMBER: US/10/858,730
; CURRENT FILING DATE: 2004-06-01
; PRIOR APPLICATION NUMBER: US 60/475,000
; PRIOR FILING DATE: 2003-05-30
; PRIOR APPLICATION NUMBER: US 60/551,860
; PRIOR FILING DATE: 2004-03-10
; NUMBER OF SEQ ID NOS: 364
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 38
; LENGTH: 2736
; TYPE: DNA
; ORGANISM: Streptomyces coelicolor
US-10-858-730-38

Query Match 3.3%; Score 64; DB 10; Length 2736;
Best Local Similarity 47.6%; Pred. No. 4,1e-06;
Matches 221; Conservative 0; Mismatches 240; Indels 3; Gaps 1;

QY 1458 CATTGAGAACTACATCGCGCGCACCATGGACGGGTGGCGGAGAACTCGCACGTGCGCAA 1517
Db 1011 CACCAAGCAGCGCTCGCCCAAGGGCACCCCGCACGAGGACGGCGCGACTACCTCGGCAC 1070
QY 1518 GCAGAACTACTTCTACTAACAATGCTACCGGCAAGTTCCTGGCGCAACTGCGCCAC 1577
Db 1071 CGCCAGCTCATCGACGACCTTCGCATCTGCAGACCTTCGTGGCGCAACACCGCGGG 1130
QY 1578 CTACTCGCGGAGGGCGCTTCGCCACCTCAAGAGTGGCGTGGTG---ACAACTGCAC 1634
Db 1131 CTGTTTCGCGAGCGGCGCTTCGCCGACCATCATCGACCTTCGGCGCTTCGCGCTCCA 1190
QY 1635 CGTCTCCACCAACTTCTTTCTATGGAGGAGCTCAAGCGCGCACCTACACCAAGGTTATCT 1694
Db 1191 GCTGCCACCATGGACGTCCGCGAGCAGCGCGACGCCCAACCAACGCGCTTCGGCCAGCT 1250
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QY 1695 GATGCACACGTGACTGGCTGGATATGCCGTGGCCAAACGAGCTGGCCGAGTGCCTGGC 1754
Db 1751 CTTGCACGGCTCGCGCAGAGAGTCTCTGGCGGTACGCCGACATGCCGCGAGTACCGCAC 1310
QY 1755 CAACGAGTGTGCGCGCGCGGCATCGTCATCTGGCGGTTCGCGCTCCCTCAGCCGCGCTA 1814
Db 1311 CAAGCTCTCGCCAAGNACTGCGCTCCGCGAGCGCTGGCCCGCCAGCCCGCGCCCGT 1370
QY 1815 CGCGAGTGTATCCAGAAAGCGGGCTTCGAGCTGGGTGATCCGCGCGGCGCACTCAGGG 1874
Db 1371 CGACGCGCGCGCGAAGAACCTTCGCGGTCTTCAGACCGCTCGCGCGCGCGCTGGAGGT 1430
QY 1875 CTACATGGAACCGCTCAACATGTATACGTCTCTTACATGSGCC 1918
Db 1431 CTTGGGCCCGAGGTCTATCGAGTCTCTACATCATCTCCATGTGCC 1474

RESULT 3
US-10-496-351-3
; Sequence 3, Application US/10496351
; Publication No. US2006008414A1
; GENERAL INFORMATION:
; APPLICANT: Floss, Heinz
; APPLICANT: Yu, Tin-Wein
; APPLICANT: Leistner, Eckard
; TITLE OF INVENTION: Biosynthetic Gene Cluster for the Maytansinoid Antitumor Agent
; TITLE OF INVENTION: Ansamitocin
; FILE REFERENCE: UWASH-06712
; CURRENT APPLICATION NUMBER: US/10/496,351
; CURRENT FILING DATE: 2004-05-19
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 4770
; TYPE: DNA
; ORGANISM: Actinosynnema pretiosum
US-10-496-351-3

Query Match 3.2%; Score 62; DB 13; Length 4770;
Best Local Similarity 44.9%; Pred. No. 1.2e-05;
Matches 236; Conservative 0; Mismatches 250; Indels 0; Gaps 0;

QY 1380 CTTCAACAAAGCCGTGCTGTGTTTCGGCGGGGGTGCAGGCAAGCAGTAGTACGCGCTGAT 1439
Db 3459 CGTCCGCGCAGCTGGCCCGCCCTCGCGCCCTCGGCGCCGACCACTCTGCTCTCAC 3518
QY 1440 CAAGCGCGACGGCATCCCATTTAGAACTACATCGCGCGCACCATGAGCGCGGTGGCGGA 1499
Db 3519 CAGCGCGCGGGCCCTCGGCCCCCGCGCGCTCGCGCCGCGCTCGCGCGCGCTGAGGCGCT 3578
QY 1500 GAACTCGCAGTGGCGCAAGCAAGAACTACTTACTACACTGCTCACCACCTCAAGAGTGGCGT 1559
Db 3579 GGGCGCGCGCTCACCACCGCCCTCGAGTGCAGCGACCGCGCGGCTTCGCCGCCCT 3638
QY 1560 GCGCGACAACTGCCCACTACCTACCTGCGAGCGGGCTTCGCCACCTCAAGAGTGGCGT 1619
Db 3639 GCTGACCGCTTGAGCGCGCGCGGCGAGCAGGTCAACCGCGCTCGTGCAACGCGGGGCGC 3698
QY 1620 GGTGGAACAACCTGACCGTCTCCACCAACTTCTTATGAGAGAGTCAAAAGCGCGCACCTA 1679
Db 3699 CAACGCCAGACCCCGCTCGCGCACACCAACCCCGAGAGCACGCGCGCGCTCCAGGCGCG 3758
QY 1680 CACCAAGTGTATTCATGGACCAAGTGTGCTGGTGGATATGCCGTGGCGCAAGAGCT 1739
Db 3759 CAAGCGCTCGCGCGCAGCACCTCGACAGTCTGGGCGGGCGCGCGCTTCGACGCGGT 3818
QY 1740 GGCGAGTGTGCGCAAGCAGAGTTGGCGCGGGCGGATCTCATCTGCGCGCTCGCGCTC 1799
Db 3819 GGTCTGTCTCTTCCAAACGCGGCGGTGTGGGCGAGCGCGCGCGCTAGCGCGC 3878
QY 1800 CCTCAGCGCGCGCTTACGCGGAGCTGTATCCAGAAAGCGGGCTTCGACGTTGCGGTGATCCG 1859
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Db 3879 GCCTCAAGCCCGCTCGACGACTGGCCCAAGCGCCGCGCGGACCGCGCGCTCGCCAC 3938

Qy 1860 CCACGCCCACTCAGGCTATCATGGACCGCGTCAACATGTACAGTCC 1905

Db 3939 CTCGTCGCGCTGGGCGCCTGGGACGCGCGGCGGATGTCCAGCGCC 3984

RESULT 4

US-10-496-351-56/c

; Sequence 56, Application US/10496351

; Publication No. US20060084141A1

; GENERAL INFORMATION:

; APPLICANT: Floss, Heinz

; APPLICANT: Yu, Tin-Wein

; APPLICANT: Leistner, Eckard

; TITLE OF INVENTION: Biosynthetic Gene Cluster for the Maytansinoid Antitumor Agent

; TITLE OF INVENTION: Anamitocin

; FILE REFERENCE: UWASH-06712

; CURRENT APPLICATION NUMBER: US/10/496,351

; CURRENT FILING DATE: 2004-05-19

; NUMBER OF SEQ ID NOS: 57

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 56

; LENGTH: 82746

; TYPE: DNA

; ORGANISM: Actinosynnema pretiosum

US-10-496-351-56

Query Match 3.2%; Score 62; DB 13; Length 82746;

Best Local Similarity 44.9%; Pred. No. 1e-05;

Matches 236; Conservative 0; Mismatches 290; Indels 0; Gaps 0;

Qy 1380 CTTCAAACAAGCCGCTGCTGTGGTTTCGGCGCGCGCTGCGCGGCAAGCAGTACGCGCTGAT 1439

Db 69521 CGTCGCGCGCAGCTGCGCGCGCGCTCGCGCGCTCGCGCGCGACCACTCGTCTCAC 68462

Qy 1440 CAAGGCGGACGGATCCCCATTGAGAACTATCGCGCGCACCATGAGCGGTGCGGA 1499

Db 68461 CAGCGCGCGCGCGCTCGCGCGCGCGCGCGCTCGCGCGCGACCTGGAGCGCT 68402

Qy 1500 GAATCGCAGTCGGCAAGCAGAACTACTTCTACTACAACTGCGCTCACCGGCAAGTTCT 1559

Db 68401 GGGCGCGCGCTCACCACCGCGCGCTCGCGCGCGCGCGCGCTCGCGCGCTCGCGCGCT 68342

Qy 1560 GCGCGCAAACTGCGCGCGCGCGCTTTCGCGCGCGCGCGCTTTCGCGCGCGCTTTCGCGCGCGCT 1619

Db 68341 GCTACCGCGCTGGAGCGCGCGCGCGCGCGCGCTGCTGCGCGCGCGCGCGCGCGCGCG 68282

Qy 1620 GTTGGACAACTGACCGCTTCCACCAACTTTCTTTCATGAGGAGCTCAAGCGCGCACCTTA 1679

Db 68281 CAACGCCAGACCCCGCTCG 68222

Qy 1680 CACCAAGTGATTTCTGATGAGACCACTGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1739

Db 68221 CAAGGCGCTCGCT 68162

Qy 1740 GGCAGGAGTCTGCT 1799

Db 68161 CGTCTGTTCTCTCAAACG 68102

Qy 1800 CCTCAGCGCGCGCTAGCGCGAGTGTATCCAGAAAGCGCGGCTTCGAGTGTGCTGATCGG 1859

Db 68101 CGCCAAAGCGCGCTCGAGCGCACTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 68042

Qy 1860 CCGCGCGCACTCAGGCTATCATGAGCGCGCTCAACATGTACAGTCC 1905

Db 68041 CTCGTCGCGCTGGGCGCGCTGGGACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 67996

RESULT 5

US-11-100-356-55

; Sequence 55, Application US/111100356

; Publication No. US20060057115A1

```

; GENERAL INFORMATION:
; APPLICANT: ZUR MEGEDE, Jan
; APPLICANT: BARNETT, Susan
; APPLICANT: LIAN, Ying
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING ANTIGENIC HIV TYPE B
; TITLE OF INVENTION: POLYPEPTIDES, POLYPEPTIDES AND USES THEREOF
; FILE REFERENCE: 2300-1621.20
; CURRENT APPLICATION NUMBER: US/11/100,356
; CURRENT FILING DATE: 2005-04-06
; PRIOR APPLICATION NUMBER: US/10/190,434
; PRIOR FILING DATE: 2002-07-05
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 55
; LENGTH: 4773
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: TatRevNefGagProtInartMut B
US-11-100-356-55

Query Match      3.1%; Score 61.2; DB 18; Length 4773;
Best Local Similarity 43.1%; Pred. No. 2e-05;
Matches 413; Conservative 0; Mismatches 533; Indels 12; Gaps 2;

QY 998 AGCTGAAGAGGTGGCCATTTCAGCAGCTGGAGTTTGAGGACGTGTGSCAGCTGTCGGCG 1057
DB 1100 AGTTGTGTCCTGGACCCCGACTACTGTGAGAGAGGCCAACGCCGGGAGAAACAAGCC 1159
QY 1058 AGGGCGGTGCACCCGCGCATTTGAGGAGCTGTACGAGAAGAAGCTGGCGCCCTTCCTGTGCG 1117
DB 1160 TGTGTGACCCCATGAGCAGCACGGCATGACGACCCCGAGAGGAGGTGCTGCTGTGGC 1219
QY 1118 AACCAGGCACACACTTCTGGTCCAAAGGGCTCTGGTACTTTCAGACGAGGCGCTGTACTACC 1177
DB 1220 GCTTTCGACAGCGCCCTGGCCCTTCCACACATGTCGCCCGAGCTGCACCCCGAGTACTACA 1279
QY 1178 AGGGCGGCATGGGCAAGCTGTGCTGGGTGCTGCAGTGCCTGGCGCTGGTGTCTGGGACTGG 1237
DB 1280 AGACTGTCAAGCTTGGCGGCCCGCCAGCGTGTCTGAGCGCGCGAGCTGGACAAGTGGG 1339
QY 1238 GCAAGACCGTCAAAGCCCTCGCCAACGCGCCCAACAATGGAGGAGCAGCGCCGCTCTGTGGG 1297
DB 1340 AGAAGATCGCCCTGCGCCCGCGGGCAAGAAGAAGTACAAGCTGAAGCACAATCGTGTGGG 1399
QY 1298 ACAGCAACATGCTCATCTCACTTCGTGAAGNACGGGCGCCCAAGCGCTGGTGTGCTGCTCG 1357
DB 1400 CCAGCGCGAGCTGGAGCGCTTCGCGCGTGAAC---CCCGGCTGTCTGGAGACACAGCGAGG 1456
QY 1358 TCAAGTTCGTGAGCCTGGTGTCTTCAAAGGCCGTGTCTGGTTTCGGCGCGCGCGTGC 1417
DB 1457 GCTGCGCCAGATCTCTGGCCAGCTCTCAGCCCAAGCTTGACACCCGAGGAGGAGCTGC 1516
QY 1418 CGGGCAAGCAGTACGCGCTGATCAAGCGCGAGCGCAATCCCAATTGAGAACTACATCGCGC 1477
DB 1517 GCAGCCTGTACAACACCGTGGCCACCCTGTACTGCGTGCACACAGCGCATCGACGTCAAGG 1576
QY 1478 GCACCATGACGCGGTGGCGGAGAACTCGACGTGCGCAAGCAGAACTACTTCTACTACA 1537
DB 1577 ACACCAAGGAGGCCCTTGGAGAAGATCGAGGAGGAGCAGAACAGTCCAAAGAAGAAGGCC 1636
QY 1538 ACTGCCTCAACCGCAAGTTTCTGCGGAGAACTGCCCCCACTACTACCTGCGGAGGCGGCT 1597
DB 1637 AGCAGCGCGCGCGCGCGCGGACCGGCAACAGCAGCAGGAGTGAGCCAGAACTACCCCA 1696
QY 1598 TCGCCCAACCTCAAGAGTGGCGTGGTGGACAACTGACCGCTCTCCACC-----AACT 1648
DB 1697 TCGTGCAAGAACCTGCAGGGGCCAGATGTTGCAACAGGCCATCAGCCCCCGCACCCCTGAACG 1756
QY 1649 TCTTCATGAGGAGAGCTCAAAGCGCGCACCTTACCAAGGTGATTCTTGATGGAACCACTGG 1708
DB 1757 CTTGGGTGAAGTGGTGGAGGAGAAGCCCTTCAGCGCCGAGGTGATCCCACTGTTCAAGCG 1816

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1709	ACTGGCTGGATATGCCCGTGGCCACAGCTGGCCGAGTGCCTGGCCAAAGCAAGTTGCGC	1768
Qy		
1817	CCCTGAGCAGGGCGCCACCCCCAGAGACTGATTGAAACACCGTGGCGGCC	1876
Db		
1769	CGGGCGCATCGTCATCTGGGGTCCGCCCTCCCTCAGCCCGCCCTACGCCGAGCTGATCC	1828
Qy		
1877	ACAGCGCCGCAATGCAGATGCTGAAGAGACCATCAACGAGGAGGCCGCCGAGTGGGACC	1936
Db		
1829	AGAAGCGGGCTTCGACGTGGTGCATCCGCGCGCCACTCAAGGGCTATACATGACCGCG	1888
Qy		
1937	CGGTGCACCCGTGCAGCCGCGCCCATCGCCCCCGCCAGATGCGGACCCCGCGGCA	1996
Db		
1889	TCAACAATGTAAGCTCCTTTCTATCATGCCCCCGCCGGAAGGGCGCCAAAGAGCAACTTA	1946
Qy		
1997	GCACATCGCCGGCACCCACAGACCCCTGCAGGAGCAGATCGGTGTGATGACCAACAA	2054
Db		

RESULT 6

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US/11-100-356-54
; Sequence 54, Application US/11100356
; Publication NO. US20060057115A1
; GENERAL INFORMATION:
; APPLICANT: ZUR MEGEDE, Jan
; APPLICANT: BARNETT, Susan
; APPLICANT: LIAN, Ying
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING ANTIGENIC HIV TYPE B
; TITLE OF INVENTION: POLYPEPTIDES, POLYPEPTIDES AND USES THEREOF
; FILE REFERENCE: 2300-1621.20
; CURRENT APPLICATION NUMBER: US/11/100,356
; CURRENT FILING DATE: 2005-04-06
; PRIOR APPLICATION NUMBER: US/10/190,434
; PRIOR FILING DATE: 2002-07-05
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 54
; LENGTH: 5283
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: description
US/11-100-356-54

```

Query Match	3.1%;	Score 61.2;	DB 18;	Length 5283;
Best Local Similarity	43.1%;	Pred. No. 1.9e-05;		
Matches 413;	Conservative 0;	Mismatches 533;	Indels 12;	Gaps 2;
Qy	998	AGCTGAAGAGGTGGCCATTACAGCAGCTGCAGATTGTAGGACGCTGTGCAGCTGTTGGCGG	1057	
Db	1106	AGCTGTGCCGTGGACCCCGACTACGTGAGGAGGCCAACCGCGGCGAACAACAGACC	1165	
Qy	1058	AGGCGGTGCACCCCGCGATTGTAGGAGCTGTACAGAGAAGACGTGGCGCCCTTCTGTGCG	1117	
Db	1166	TGCTGCACCCCATGAGCCAGCAGCGCATGACAGACCCCGAAGAGGAGTGTGTTGTGCG	1225	
Qy	1118	AAACACAGCCACAACCTTCTGGTCCAAAGCGCCTCTGGTACTTCCAGCAGCGGCTGTACTACC	1177	
Db	1226	GCITTCGACAGCGCGCTGGCCCTTCACACATGCCCCGAGCTGCACCCCGAGTACTACA	1285	
Qy	1178	AGGCGGCATGGGCAAGCTGTCTGGGTGCTGCAGTGCCTGGCGCTGGTGTCTGGGACTGG	1237	
Db	1286	AGGACTGCCTCGAGGGCGCCCGGCCAGCGTGTGAGCGCGCGAGCTGGACAAGTGGG	1345	
Qy	1238	GCAGAACGTCAGCGGCTGCCAACCGCCCCAACATGGAGAGGACGCGCGCTCTGTGGG	1297	
Db	1346	AGAAGATCCGCGCTGCGCCCCCGGGCGCAAGAAGATACAAGCTGAAGCAATCGTGTGGG	1405	
Qy	1298	ACAGCAACATGCTCATCCAATTCGTGAAGAACGGGCCCCAAGCGCTGGTGTGGTGTTCG	1357	
Db	1406	CCAGCCCGAGCTGGAGCGCTTCGCCGTGAAC---CCCGGCTGTCTGGACACCGCAGG	1462	
Qy	1358	TCAAGTTTCGTGAAGCTGGTCTCTTCAACAAGGCGCTGTGTGGTTCGGCGGGCGGTGC	1417	

1463	DB	GCTGCCGCCAGATCTCTGGGCCACGCTGCAGCCCTGAGCTGCAGACGGGACGAGGAGCTGC	1522
1418	QY	CGGCGAAGCAGTAGTACGGGCTGATCAAGGCGGACGGGCATCCCCATTGAGAACTACATCGCGC	1477
1523	DB	GCAGCCTGTACACACCGTGGCCACCTGTACTCTGGTGACACGACGCATCGACGTCAAGG	1582
1478	QY	GCACCATGGACGCGTGGGGAGAACTCGCACGTGGCGAAGCAACTCTTCTACTTACA	1537
1583	DB	ACACCAAGGAGGCCCTCGAGAAATCGAGGAGGACAGAACTGTCAGGAAGAAGGCCCC	1642
1538	QY	ACTGCCTCACCGGCAAGTTCTTGGGGACAACTGCCCCACCTACCTTGGCGGAGGCGGCCT	1597
1643	DB	AGCAGGCCGCGCGCGCGGCACCGGCACACGACGCCAGGTGAGCCAGAACTACCCCCA	1702
1598	QY	TCCGCCACCTCAAGAGTGGGTGGTGACAACTGACCGTCTCCACC-----AACT	1648
1703	DB	TCGTGCAGAACCTTGCAGGGCCAGATGGTGCACACAGGCCCATCAGCCCCGACCCCTGACG	1762
1649	QY	TCTTCTGAGGAGACTCAAAAGCGCGCACCTTACACCAAGGTGATTCTGTATGGACCACTGG	1708
1763	DB	CCTGGGTGAAGGTGGTGAGAGAGGCCCTTCAGCCCCGAGGTGATCCCCATGTTTCAGCG	1822
1709	QY	ACTGGCTGGATATGCCGTGGCCAAACAGCTGGCGGAGTGCCCTGGGCCAACGACAGGTTGCGC	1768
1823	DB	CCCTGACGAGGGCGCCACCCCGCAGACCTGAACACGATGTTTGAACACCGTGGGCGGCC	1882
1769	QY	CGGGCGCATCGTCACTTGGGGCTCCGCTCCCTCAGCCCGCCCTTAGCCCGAGCTGATCC	1828
1883	DB	ACCAGGCCGCCATGTCAGATCTGAAGAGAGACCATCAACGAGGAGGCCCGCCGATGGGACC	1942
1829	QY	AGAAGGGGGCTTCGACGTGCGTGTATCCCGCGCCACTCAGGGGTACATGGAACCGCG	1888
1943	DB	CGGTGCACCCGTGCACGCGGGCCCCATGCCCCCCGGCCAGATGGCGAGCCCGCGGCA	2002
1889	QY	TCAACATGTACAGTCTCTTACATGGCCCGCCGGAGGGCGCCAGAAAGGACAACTTA	1946
2003	DB	GCACATATCGCCGGCACACACGACACCCCTGCAGGAGCAGATCGGTGTGATCACCACAA	2060

RESULT 7

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US-11-096-568A-1077
; Sequence 1077, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fr
; TITLE OF INVENTION: Sequence-Determined DNA Fr
; TITLE OF INVENTION: Sequence-Determined DNA Fr
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 1077
; LENGTH: 1325
; TYPE: DNA
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(1325)
; OTHER INFORMATION: Ceres Seq. ID NO. 13599631
US-11-096-568A-1077

```

	Query Match	3.1%	Score 60.8;	DB 18;	Length 1325;
	Best Local Similarity	45.4%;	Pred. No. 2.7e-05;		
	Matches 258;	Conservative	0; Mismatches 307;	Indels 3;	Gaps 1;
1218	GGCCGTGTGTGGGACTGGGCAAGACCGTCAAGGGCTTCCCAACGGGCCACAAATGGA				12777
293	GGCGTGGGGTTTCGGACAGCCACGGCGACGTGGCCCGGATCCAGTGTGCCACATCGG				352
1278	GGAGCAGCGCGTGTGTGGGACAGCAACATGCTCATTCATCTGTGAAGAACGGGCCCAA				1337
353	CCTCCACGGCGCGACCTTCGTGTGCGAGTGTCTCATCAAGAACCACCAACCGGTGTGCCAT				412

	Query Match	3.1%	Score 59.6	DB 18	Length 1347
	Best Local Similarity	47.2%	Pred. No. 5.2e-05		
	Matches 253	Conservative 0	Mismatches 274	Indels 9	Gaps 2
Qy	1316	ACTTCGTGAAGAACGGGCCCAAGCCGCTGTGTGTGGCTGTTCGTCAAGTTCGTGAGCGCTGG	1375		
Db	351	ACAAAGGTGGACAGCCGCTCAAGAGACATGGCGGTGGTGTGAAGACAGCGCGGTTCACCTGG	410		
Qy	1376	TGCTCTTTCAACAAGCGCGTGTGTGGTTTCGGCGCGCGCGTCCGGGCCAAGCAGTACGCGC	1435		
Db	411	ACGAGCGGTGGACGCCATCGGTTCGTTCGCCACCTCTGCCCGGGGAGCACTGCGAGG	470		
Qy	1436	TGATCAAGCGGGACGGC---ATCCCCATTGAGAACTCATTCGGCGCGCACCATCGAAGCGG	1492		
Db	471	AGTCCCTTGGACACATCCTGCTGCACCTCTACAAGGCCAGCGGGCGCCCAAGAGAGAGA	530		
Qy	1493	TGGCGGAGAACTCGCACGTGGCGCAAGCAGAACTACTTCTACTCAACTGCTCTCACCGGCA	1552		

```

FILE REFERENCE: 2300-1621-20
CURRENT APPLICATION NUMBER: US/11/100,356
CURRENT FILING DATE: 2005-04-06
PRIORITY APPLICATION NUMBER: US/10/190,434
PRIOR FILING DATE: 2002-07-05
NUMBER OF SEQ ID NOS: 68
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 53
LENGTH: 2799
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: TatRevNefGag B
US-11-100-356-53

```

```
Db 1400 CCAAGCCGAGCTGGAGCGCTTCGCGTGAAC---CCGCGCTGCTGGAGACCGAGG 1456
QY 1358 TCAAGTTTGTAGCCTGTGTCTTCAACAGAGCCGTGCTGTGTGTTCGGCGCGCGGTGC 1417
Db 1457 GCTGCGCGCAGATCTGGCGCCAGCTGCAAGCCAGCTGCAAGCCGAGCGGAGAGTGC 1516
QY 1418 CGGCAAGCAGTACCGCTGATCAAGGCGGAGCGGATCCCATTTGAGAACTACATCGCGC 1477
Db 1517 GGAGCTGTACAAACCGTGGCCACCTGTATCTGGTGCACACAGGCGATCGACGTTCAAGG 1576
QY 1478 GCACCATGAGCGGCTGGCGAGAACTCGCAGTGGCGAAGCAGAACTTACTTCTACTACA 1537
Db 1577 ACACCAAGGAGCCCTGGAGAAGATCGAGGAGGACAGAACAGTGTCAAGAGAGGCC 1636
QY 1538 ACTGCTCACCAGCAAGTTCTGCGCGAACAAGTGGCCCACTTCTGCGCGAGGCGGCT 1597
Db 1637 AGCAGCGCGCGCGCGCGCGCACCGGCAACAGCAGCAGCGTGAAGCCAGAACTACCCCA 1696
QY 1598 TCGCCACCCTCAAGAGTGGCGTGGAGAACCTGACCGTCTCCACG-----AACT 1648
Db 1697 TCGTGCAGAACTGAGGCGCAGATGGTGCACAGGCCATCAGCCCGCGCACCTGGAACG 1756
QY 1649 TCTTCATGAGGAGCTCAAGCGCGCACCTACACCAAGGTGATTTCTGATGGACCACTGG 1708
Db 1757 CTGSGTGAAGTGTGAGGAGAGGCTTCAGCCCGAGGTGATCCCATGTTTCAGCG 1816
QY 1709 ACTGCTGGATATGCCCTGGCGAACAGAGCTGGCGAGTGGCTGGCGAAGCAGTTGGCG 1768
Db 1817 CCTGAGCGAGGCGGCCACCCCGCAGGACCTGAACACAGATGTTGAACACCGTGGCGGCC 1876
QY 1769 CGGGCGGATGTCATCTGGCGCTCCGCTCCCTCAGCGCCGCTTACGCGGAGCTGATCC 1828
Db 1877 ACCAGCGCCATGATGATGCTGAAGAGACCATCAACAGAGGCGCCGAGTGGAGC 1936
QY 1829 AGAAGCGGGCTTGACGCTGGCTGCTCCGCGCGCCACTCAGGGCTTACATGGACCGCG 1888
Db 1937 GCGTGACCCGCTGACCGCGGCCCATCGCCCGCGCAGATGCGCGAGCCCGCGCA 1996
QY 1889 TCAACATGATAGTCTCTTCTACATGGCCCGCGGAGAGGCGGCCAAGAGCAACTA 1946
Db 1997 GCGACATCGCGCGCACCAACGACCTCTGAGGAGCAGATCGGTGGATGATGACCAAC 2054
```

RESULT 10

```
US-11-096-568A-26187
; Sequence 26187, Application US/11096568A
; Publication No. US20060048240A1
```

GENERAL INFORMATION:

```
; APPLICANT: Alexandrov, Nikolai et al.
```

```
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
```

```
; TITLE OF INVENTION: thereby
```

```
; FILE REFERENCE: 2750-1592PUS2
```

```
; CURRENT APPLICATION NUMBER: US/11/096, 568A
```

```
; CURRENT FILING DATE: 2005-04-01
```

```
; NUMBER OF SEQ ID NOS: 34471
```

```
; SEQ ID NO 26187
```

```
; LENGTH: 1599
```

```
; TYPE: DNA
```

```
; ORGANISM: Zea mays subsp. mays
```

```
; FEATURE:
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```
; NAME/KEY: misc.feature
```

```
; LOCATION: (1)..(1599)
```

```
; OTHER INFORMATION: Ceres Seq. ID no. 13498780
```

```
US-11-096-568A-26187
```

Query Match 3.0%; Score 57.8; DB 18; Length 1599;

Best Local Similarity 44.3%; Pred. No. 0.00014;

Matches 236; Conservative 0; Mismatches 297; Indels 0; Gaps 0;

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QY 1408 GCGCGCTGCGCGGCAAGCAGTACGCGCTGTATCAAGGCGGACGGCATCCCATTTGAGAAC 1467
Db 277 GGGTACATGCGCGCGCGCTCTTACGACCTGGACGCGTCCAAAGTACGGCACCCACGCGAG 336
```

```
QY 1468 TACATCGCGCGCACCATGGACGGCGTGGCGSAGAACTCGCACGTTGCGCAAGCAGAACTAC 1527
Db 337 CTAAGTGTCTTCAACGGCGGCTTCAACGCCAAGGGCTCAAGTGGTGGCGGAGTGTG 396
QY 1528 TTCTACTAACATGCTCCTCACCGGCAAGTTCTTGGCGGACAACTGCCCACTTCTGCGC 1587
Db 397 ATCAACACACGCTGGCGGACTACAAGGACGGCGCGGCATCTACTGCGTCTTCAGGGC 456
QY 1588 GAGCGGCTTTCGCGACCTCAAGAGTGGGTGTGTGACAACTGACCGTCTCCACCAAC 1647
Db 457 GGCACGCCGACAGCCCTCGACTGGGGGCCCGACATGATCTCTAGCGACACACGCGAG 516
QY 1648 TTCTTCATGAGGAGCTCAAGCGCGCACCTTACACCAAGGTGATTTCTGATGACCACTG 1707
Db 517 TACTCCAAAGCGCGGGGCAACCGGACACAGGGGCGGACTTCGGCGCGCGCCGACATC 576
QY 1708 GACTGGCTGGATATGCCGTGGCCAAAGAGTGGCGCGAGTGGCTTGGCCAAAGCAGGTTGCG 1767
Db 577 GACCACCTCAACCCGCGCTGACAGCAGGAGCTCTCGGACTGGCTCAACTGGCTCAAGTCC 636
QY 1768 CCGGGCGCATGTCATCTGGCGCTCGCCTCGCTCCTCAGCCCGCCCTAGCCGAGCTGATC 1827
Db 637 GACTCGGCTTCGACGGCTGGCGCTCGACTTCGCCAAGGGCTACTCGCGCGCGCTGCCC 696
QY 1828 CAGAAGCGGGCTTCGACGCTGCGCTGATCGCGCGCCACTCAGGGCTTACATGGACCGC 1887
Db 697 AAGTGTAGCTGCACAGCAGCGCCCGCCACTTCTGCTGCGCGGAGATATGGAGTCCCTC 756
QY 1888 GTCAACATGTACAGCTCTCTTCTACATGGCGCGCGGAAAGCGGCCAAGAGGA 1940
Db 757 CACTACGACGGCAACGGCGAGCGCTCGAGCAACCGAGGACCGCGACAGCAGGA 809
```

RESULT 11

```
US-11-096-568A-20988
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```
; Sequence 20988, Application US/11096568A
```

```
; Publication No. US20060048240A1
```

```
; GENERAL INFORMATION:
```

```
; APPLICANT: Alexandrov, Nikolai et al.
```

```
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
```

```
; TITLE OF INVENTION: thereby
```

```
; FILE REFERENCE: 2750-1592PUS2
```

```
; CURRENT APPLICATION NUMBER: US/11/096, 568A
```

```
; CURRENT FILING DATE: 2005-04-01
```

```
; NUMBER OF SEQ ID NOS: 34471
```

```
; SEQ ID NO 20988
```

```
; LENGTH: 1444
```

```
; TYPE: DNA
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```
; ORGANISM: Zea mays subsp. mays
```

```
; FEATURE:
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```
; NAME/KEY: misc.feature
```

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; LOCATION: (1)..(1444)
```

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; OTHER INFORMATION: Ceres Seq. ID no. 12391561
```

```
US-11-096-568A-20988
```

Query Match 3.0%; Score 57.6; DB 18; Length 1444;

Best Local Similarity 46.2%; Pred. No. 0.00016;

Matches 192; Conservative 0; Mismatches 224; Indels 0; Gaps 0;

```
QY 1527 CTTCTACTACAACTGCGCTCACCGGCAAGTTCTCGCGGACAACTGCCCACTTACCTGCG 1586
Db 510 CTTCTGCGCTTACGCTCAGCTTCTGCAITGTGATATCTTCCCGGACCTCTCTGCGG 569
QY 1587 CGAGGCGGCTTCCGCCACCTCAAGAGTGGGTGTGGAACCTGACCGTCTCCACCAA 1646
Db 570 CGACCCGCGCTTACCGCGCGGCGGCAACACCTTCTTCTCATGGAACAAAGGACAA 629
QY 1647 CTTCTTATGAGGAGCTCAAGCGCGCACCTTACACCAAGGTGATTTCTGATGGACCACT 1706
Db 630 GGACTTCTGCTCTCTCGGACGCGGCTCTCAATCAACGCCCACTTCTATCGGCAACA 689
QY 1707 GGACTGGCTGGATATGCCGTGGCCAAACGAGCTGCGCGGCTGTGGCCAAAGCAGGTTGC 1766
```



```
Db 690 CAACCGGCGCTCAACCGGACCTTCACTGGGTGAGGGCTGGGGTACCTTGGTGGC 749
Qy 1767 GCGGGCGGCGATCGTCACTTGGCGCTCGCGCTCCCTCAGCCCGCCTACGGCGAGCTGAT 1826
Db 750 ACCAGCGCGCGCGGAGCGCACCGCTCTACGTTCGGCGCGCGCAGGCGCGCGAGTG 809
Qy 1827 CCAGAAGCGGCGCTTCGAGCTGGCTGTGANTCCGCGCGCGCACTCAGGGGTACATGAGCG 1886
Db 810 GGACGAGGAGGACGACCACTCCAGCTCACCTTGGACCGCGAGCGCGCTCGAGCTCGAGCG 869
Qy 1887 CGTCAACATGTACAGCTCTCTTACATGCGCGCGCGAGGGCGCCAAAGAGGACA 1942
Db 870 CGTCAAGAACGCGCGCTGGCGCTCCAGGCGCTCCCGGGGCTCTCCGTCAACGGCA 925

RESULT 12
US-11-166-609-1
; Sequence 1, Application US/11166609
; Publication No. US20060015968A1
; GENERAL INFORMATION:
; APPLICANT: ALBERTSEN, MARC C.
; APPLICANT: FOX, TIM
; APPLICANT: HUFFMAN, GARY
; APPLICANT: TRIMNELL, MARY
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES MEDIATING MALE FERTILITY AND
; TITLE OF INVENTION: METHOD OF USING SAME
; FILE REFERENCE: 1148CR
; CURRENT APPLICATION NUMBER: US/11/166,609
; CURRENT FILING DATE: 2005-06-24
; PRIOR APPLICATION NUMBER: 10/412,000
; PRIOR FILING DATE: 2003-04-11
; PRIOR APPLICATION NUMBER: 09/670,153
; PRIOR FILING DATE: 2000-09-26
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 1
; LENGTH: 1906
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1638)
US-11-166-609-1

Query Match 2.9%; Score 57.2; DB 17; Length 1906;
Best Local Similarity 43.1%; Pred. No. 0.0002;
Matches 275; Conservative 0; Mismatches 363; Indels 0; Gaps 0;

Qy 908 GCGGCGGTGCAATGCCCTGAACCTGCTGGTGCAGGGGGCGCGCAGGTGGTGGTGG 967
Db 911 GCGGCGGTTCGGGAGCATGAAGACCTCCGGAGCTGGTGTCAACTTGTGTATCGCG 970

Qy 968 ACTGCAACCCCGCAGTCGCGGCTTCTGGAGCTGAAGAAGTGGCCATTCAGCGAGTGG 1027
Db 971 GCGGGAGACGACGCGGACGAGCTGTCTGTGTTTCAACGACATGGCCATGTCCCAACCG 1030

Qy 1028 AGTTTGAGGACGTGGCAGCTGTTTCGGGAGGGCGTGCACCCGCGCATTCAGGAGCTGT 1087
Db 1031 ACGTGGCCGAGAAGCTGCGCGCGAGCTGTGCGCGTTTCGAGCGGAGCGCGCGCGGAG 1090

Qy 1088 ACGAGAAGAAGCTGGCGCGCTTCTCTGTGCGAAACGAGCGCAACACTTCTGGTCCAAGCGCC 1147
Db 1091 AGGGGCTCAGCTGTGTCTTCTGGCGGGCGGTGACGCGAGCAAGCGGTTCGCGCGCC 1150

Qy 1148 TCTGTACTTCCAGCACCGGCTGTACTACAGGGCGGCGATGGGCAAGCTGTGCTGGGTGC 1207
Db 1151 GCGTGGCGAGTTTCGGGGCTCTCTACCTACGACAGCGCTCGGCAAGCTGTGCTACCTCC 1210

Qy 1208 TGCAGTGCCTGGCGGTGTGTGGACTGGGCAAGACCGTCAAGCGCTTCGCCACGCGC 1267
Db 1211 ACGCTGCGTCAACGAGAGCTGCTCGCGCTGTATCCCGCGCGTCCCTCAGGACCCCAAGGGGA 1270
```

```
Qy 1268 CCACAATGGAGGAGGCGCGCTGTGGGACAGCAACATGCTCATCCACTTCGTGAAGA 1327
Db 1271 TCCTGGAGGACGAGCTGTGCCGAGCGGACGGAAGGTGAGGGCGGCGGATGGTGAGCT 1330
Qy 1328 ACGGCGCCCAAGCGCTGGTGTGGCTGTTTCGTCAAGTTTCGTGAGCCTGGTGTCTTCAACA 1387
Db 1331 ACGTGGCTTACTCATGGGGCGGATGGAGTACACTGGGGCCCCGACGCGGGGAGCTTCC 1390
Qy 1388 AGGCGGTGCTGTGGTTGGCGCGCGCTGCGGCAAGCACTACGCGTGTGATCAAGGGCG 1447
Db 1391 GGCGGAGCGGTGGATCAACGAGGATGGCGGCTTCGCAACGCGCTGCGGTTCAAGTTCA 1450
Qy 1448 ACGCATCCCATTTAGAACTACATCGCGCGCACCATGGAGCGGTGCGGGAGACTGCG 1507
Db 1451 CGGCGTTCCAGGGCGGGCGGAGATCTGCTGGGCAAGGACTCGGCGTACTCTGCAGATGA 1510
Qy 1508 ACGTGGCGCAAGCAGAACTACTTCTACTACAACTGCCTC 1545
Db 1511 AGATGGCGCTGGCCATCTCTTCGCTTCTACAGCTTC 1548

RESULT 13
US-10-858-730-142
; Sequence 142, Application US/10858730
; Publication No. US20050255568A1
; GENERAL INFORMATION:
; APPLICANT: Bailey, Richard B.
; APPLICANT: Blomquist, Paul
; APPLICANT: Doten, Reed
; APPLICANT: Driggers, Edward M.
; APPLICANT: Madden, Kevin T.
; APPLICANT: O'Leary, Jessica
; APPLICANT: O'Toole, George
; APPLICANT: Trueheart, Joshua
; APPLICANT: Walbridge, Michael J.
; APPLICANT: Yorgey, Peter S.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR AMINO ACID
; TITLE OF INVENTION: PRODUCTION
; FILE REFERENCE: 14184-030001
; CURRENT APPLICATION NUMBER: US/10/858,730
; CURRENT FILING DATE: 2004-06-01
; PRIOR APPLICATION NUMBER: US 60/475,000
; PRIOR FILING DATE: 2003-05-30
; PRIOR APPLICATION NUMBER: US 60/551,860
; PRIOR FILING DATE: 2004-03-10
; NUMBER OF SEQ ID NOS: 364
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 142
; LENGTH: 3513
; TYPE: DNA
; ORGANISM: Streptomyces coelicolor
US-10-858-730-142

Query Match 2.9%; Score 56.2; DB 10; Length 3513;
Best Local Similarity 44.6%; Pred. No. 0.00034;
Matches 266; Conservative 0; Mismatches 328; Indels 3; Gaps 1;
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Qy 1146 CCTCTGTGTACTTCCAGACGAGCGCTGTACTACAGCGGGCATGGCAAGCTGTGCTGGGT 1205
Db 1179 CCTCTGTGTCACTACGTTCGGCGCGGACGGCGTCCGCAATGAGGAACTGGCGGCGCG 1238
Qy 1206 GCTGCAGTGCCTGGCGCGCTGTGCTGGGACTGGGCAAGACCGCTCAAGCGCTTCGCCAACGC 1265
Db 1239 GTTCGCCACCGCTCCACGCTGCCGATCGTCTCCAGCTCCACCGAGGTTCGAGCTCATCG 1298
Qy 1266 GCCCAATGAGGAGAGAGCGCGCTGTGTGGGACAGCAATGCTCATCTCAGCTTCGTA 1325
Db 1299 GGCGGCGCTGAGAAAGCTCGGCGCGCGGTGATCAACTCGGTCAACTACGAGACGG 1358
Qy 1326 GAACGGGCGCCAAAGCGCTGTGCTGTTCGTCAGTTTCGTAGCCCTGCTCTTCAA 1385
Db 1359 GGCGGCGCGCGAGTCCCGGTTCCGCCGCGCTCAGAACTCCCGCGGAGACGGCGCGCG 1418
```

QY 1386 CAAGCGGTGTGTGGTTCGGCGGGGTGTCGGCGGAAGCAGTACGGCTGATCAAGGC 1445
Db 1419 GCTGATCGCGTGAACATCGAGAGTGGGAGAGCCCGGACCGCGGAGAGAGGTGGA 1478
QY 1446 GGACGGCATCCCATTTGAGAACTACATCGCGCGCACCATGATGACGGCGTGGGAGAACTC 1505
Db 1479 GATCGCGAAGCGGTCTATCGAGGACCTCACCGGAACATGGGGCATCCACGAGTCCGACAT 1538
QY 1506 GCAGTGGGGAAGAGAACTACTTCTACTACAACTGCTCTACCGGCAAGTTCCTGGGGA 1565
Db 1539 CCTGCTGACTGCGCTGACTTTCACCATCTGCACCGGCC--AGGAGGAGTCCCGCAAGGA 1595
QY 1566 CAATGCCCCACCTACCTGCGGAGGGCGCTTCGCCACCTCAAGAGTGGCGTGTGGA 1625
Db 1596 CGGCTGGCCACCATCGAGGACATCCGGGAATCCGGGAATCAAGCGGCGCCACCGGACGTGCAGAC 1655
QY 1626 CAACCTGACCGTCTCCACCAACTTCTTCATGAGGAGCTCAAGCGGCGCACCTACACCAA 1685
Db 1656 CACGCTCGGCCTGTGCAACATCTCTTCGGCCTCAACCGGCGCCCGCATCTGCTCAA 1715
QY 1686 GGTGATCTGATGACACACGTGAGTGTGCTGATGATGCCGTGGCCCAACGAGTGGC 1742
Db 1716 CTCGGTCTTCTCGACCAATGCGTCAAGCGCGGCTGGACTCGGCCCATCGTGCACGC 1772

RESULT 14

US-11-183-624-1
; Sequence 1, Application US/11183624
; Publication No. US20050255518A1
; GENERAL INFORMATION:
; APPLICANT: Silos-Santiago, Inmaculada
; TITLE OF INVENTION: Methods and compositions for the
; FILE OF INVENTION: treatment and diagnosis of pain disorders using 46556
; FILE REFERENCE: MP101-272P1RM
; CURRENT APPLICATION NUMBER: US/11/183,624
; PRIOR FILING DATE: 2005-07-18
; PRIOR APPLICATION NUMBER: US/10/281,866
; PRIOR FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: 60/335,078
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 4282
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-183-624-1

Query Match 2.9%; Score 56; DB 17; Length 4282;
Best Local Similarity 44.2%; Pred. No. 0.00038;
Matches 282; Conservative 0; Mismatches 350; Indels 6; Gaps 1;
QY 1024 CTGGAGTTTGAAGGACGTGTGGCAGCTGTTCCGGCGAGGGCGTGCACCCCGCATTTGAGGAG 1083
Db 766 CAGGTGTGGAGGGCGCTGCTGACCTGTCTTCTCCGGTGTGGTGTATTCGCTGG 825
QY 1084 CTGTACGAGAAAGAGCTGGCGCCCTTCTGTGCGAAACACGACCAAACTTCTGTGTCCAG 1143
Db 826 ATGGCCGACAAAGCGCTCTCTTCTACAAAGTACGTGTACAAAGCGCTACCGCACCGACCCA 885
QY 1144 CGCCTCTGTGTAATCCACGACGGCTGTACTACGAGGGCGCATGGGCAAGCTGTGTGG 1203
Db 886 CGCAGCGGCATCATATAGGCGCGCAGGGCGCACCCCGAAGAGCATCGAGCTGACGGC 945
QY 1204 GTGCTGTGAGTCTGCGCGTGTGTGGGACTGGGCAAGACCGTCAAGCGCTCGCCCAAC 1263
Db 946 ACGTTCGTGGCGCGAGGCCCGCCAGGTGAGTGTGGCGCTGGGCGCGGCCCGCGCAG 1005
QY 1264 GCGCCCAAAATGAGGAGACGAGCGCTGTGTGGGACAGCAATGCTCATCTGCTGTG 1323
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US-11-183-624-3
; Sequence 3, Application US/11183624
; Publication No. US20050255518A1
; GENERAL INFORMATION:
; APPLICANT: Silos-Santiago, Inmaculada
; TITLE OF INVENTION: Methods and compositions for the
; FILE OF INVENTION: treatment and diagnosis of pain disorders using 46556
; FILE REFERENCE: MP101-272P1RM
; CURRENT APPLICATION NUMBER: US/11/183,624
; PRIOR FILING DATE: 2005-07-18
; PRIOR APPLICATION NUMBER: US/10/281,866
; PRIOR FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: 60/335,078
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 4282
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (94)...(2859)
US-11-183-624-3

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Job time : 955 secs

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GenCore version 5.1.7
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Run on: May 5, 2006, 07:49:43 ; Search time 7.4 Seconds
(without alignments)
4350.528 Million cell updates/sec

Title: US-10-620-914-44

Perfect score: 3619

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Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 1144120

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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C 2	352	9.7	310	2	US-09-248-796A-21233
C 3	332.5	9.2	663	2	US-09-252-991A-30843
C 4	332	9.2	536	2	US-09-252-991A-16754
C 5	326.5	9.0	681	2	US-09-252-991A-24567
C 6	324	9.0	2294	2	US-09-252-991A-17231
C 7	323	8.9	638	2	US-09-252-991A-27068
C 8	317.5	8.8	467	2	US-09-252-991A-18296
C 9	316.5	8.7	1706	2	US-09-252-991A-31760
C 10	310	8.6	1073	2	US-09-252-991A-27341
C 11	309	8.5	798	2	US-09-252-991A-23774
C 12	308	8.5	1064	2	US-09-252-991A-17508

13	307.5	8.5	957	2	US-09-252-991A-20408	Sequence 20408, A
C 14	303	8.4	783	2	US-09-252-991A-18035	Sequence 18035, A
C 15	302	8.3	863	2	US-09-252-991A-26099	Sequence 26099, A
C 16	300.5	8.3	369	2	US-09-252-991A-25394	Sequence 25394, A
C 17	300	8.3	882	2	US-09-413-814-78	Sequence 78, Appl
C 18	299	8.3	511	2	US-09-252-991A-26078	Sequence 26078, A
C 19	298.5	8.2	720	2	US-09-252-991A-31915	Sequence 31915, A
C 20	298	8.2	568	2	US-09-252-991A-23264	Sequence 23264, A
C 21	297.5	8.2	885	2	US-09-252-991A-26129	Sequence 26129, A
C 22	295.5	8.2	885	2	US-09-252-991A-26129	Sequence 26129, A
C 23	295.5	8.2	1427	2	US-09-252-991A-20577	Sequence 20577, A
C 24	295.5	8.2	1476	2	US-09-252-991A-29427	Sequence 29427, A
C 25	295	8.2	686	2	US-09-252-991A-21221	Sequence 21221, A
C 26	295	8.2	783	2	US-09-252-991A-18035	Sequence 18035, A
C 27	295	8.2	882	2	US-09-413-814-78	Sequence 78, Appl
C 28	293.5	8.1	1008	2	US-09-252-991A-29419	Sequence 29419, A
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C 30	291	8.0	801	2	US-09-252-991A-29274	Sequence 29274, A
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C 33	289	8.0	774	2	US-09-252-991A-16789	Sequence 16789, A
C 34	288	8.0	863	2	US-09-252-991A-26099	Sequence 26099, A
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C 38	287.5	7.9	977	2	US-09-252-991A-16655	Sequence 16655, A
C 39	286.5	7.9	577	2	US-09-252-991A-25632	Sequence 25632, A
C 40	285.5	7.9	596	2	US-09-252-991A-18875	Sequence 18875, A
C 41	285.5	7.9	1053	2	US-09-252-991A-26140	Sequence 26140, A
C 42	284.5	7.9	691	2	US-09-252-991A-31413	Sequence 31413, A
C 43	284.5	7.9	1008	2	US-09-252-991A-29419	Sequence 29419, A
C 44	284.5	7.9	1520	2	US-09-252-991A-17501	Sequence 17501, A
C 45	283.5	7.8	419	2	US-09-252-991A-31734	Sequence 31734, A

ALIGNMENTS

RESULT 1
US-09-252-991A-30843
; Sequence 30843, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR FILING DATE: 1999-02-18
; PRIOR FILING DATE: 1998-02-18
; PRIOR FILING DATE: 1998-02-18
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 30843
; LENGTH: 663
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-30843

Alignment Scores:
Pred. No.: 2.18e-19 Length: 663
Score: 374.50 Matches: 211
Percent Similarity: 33.2% Conservative: 34
Best Local Similarity: 28.6% Mismatches: 231
Query Match: 10.3% Indels: 263
DB: 2 Gaps: 49

US-10-620-914-44 (1-1947) x US-09-252-991A-30843 (1-663)

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QY 1558 ---GGAACCTCCCGGTGAGGCAGTTGT-----AGTAGA 1529
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US-09-248-796A-21233
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Db	583	AlaAlaProAlaGlyProThrPro	600
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Db	601	ProSerAlaProProArgProAlaArgArgArgValArgTrpProTrpArgSerAlaArg	620
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RESULT 4
US-09-252-391A-16754
; Sequence 16754, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND
; TITLE OF INVENTION: AERUGINOSA FOR DIA
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,9

Qy	1276	CCATTGTGGCGGCTTGGCGAGCGCTTGACGGTCTTGC-----CCAGTCCGAGCA	1226
Db	216	erSerMetAlaArgLeuAlaAlaArgPheSer-SerSerMetGluProProProAla	235
Qy	1225	CCAGGCCAGGCACTGCAGCACCACCGACACAGCTTGCCCATGCCCGCTGTAGTACAGGC	1166
Db	236	MetArgArgAsnAlaArgThrArgThrArgAlaArgGlySerProGlyGlySerThrGly	255
Qy	1165	CGTGTGGAAAGTACCAGAGCGCTTGGACCAGAAAGTTGTGGCTGGTTGGCACGGAAGG	1106
Db	256	ArgGlyGlyTyrThrArgGly-----	262
Qy	1105	AGCCAGCTTCTTCTCGTACAGCT---CCTCAATGCGCGGTGCA-----	1064
Db	263	SerSerAlaSerProArgProAlaThrProAlaAlaAlaGlyAlaArgAlaArgAla	282
Qy	1063	-----CGCCCTGCCCAACAGCTGCCACAGCTCTCTCAAACTCCAGCTGTGTAA	1016
Db	283	ArgProArgProArgProAlaArgThrCysArgProAlaProCysArgProGly-----	300
Qy	1015	TGGCCACTTCTTTCAGTCCA-----	983
Db	301	-----ProSerAlaAlaProArgArgHisArgArgArgAspArgArgArgProSer	318
Qy	982	CGCGGGGTTTGCAGTCCACGG-----ACACCACCTGGCGCGCCCTGCA-----	938
Db	319	GlySerGlyCysGlyGlyProAlaGlyThrProSerGlyArgValProGlyArgArgVal	338
Qy	937	-----CGACGAGTTTCAGGGCATTCCAGCCGC	911
Db	339	GlyArgAlaGlyAsnCysAlaArgAlaGlyArgProAlaGlyAlaAlaArgAlaArg	358
Qy	910	-----CGCTAGTCAGGTCAGCACCGTGTCTTGGGTTGATCTCCATCA	866
Db	359	ProGlyArgProValArgArgAlaLeuAlaGlyCys-----	371
Qy	865	CTCTCCATATCCGCTCGGGTCTCTCCACGACTTCGCTGTACAGAAAGTGGCGGGAACA	806
Db	372	---ProValProAlaAlaGlyArgProGlyTyrSerArgProAlaArgArgSerGly---	389
Qy	805	TGGCGGCGCTCCACGCGCTCTCTGTGANGGCGT-----GCCCAACGCTGG	758
Db	390	-----SerProArgProValAlaGlyArgAspProSerProGlyArgArgAla	406
Qy	757	GCAGCGGCCAATCCACACGTAGTGGGdCGGCAGCCACGCGCAGTGGGATCGAAC	698
Db	407	AlaGlyAlaGlySerValAlaAsp-----	414
Qy	697	CTTGGTGTCTCTCCACACGCGCTCCAGCTTCTGCTCCAGTAGGCGCGCGCTCGG	638
Db	415	-----SerAlaProGlyThrArgArgAlaArg	423
Qy	637	GGCCGANGTCAATGTTGATGTCGAAGCA-----TCGATCCGCCAAGAAAC	590
Db	424	AlaAlaAlaGlyCysGlyArgSerArgArgAlaArgLysAlaAlaValProArgArgSer	443
Qy	589	GGCGCAGCAGGCACTCTGGCGCAGGGGAGGTCTGTACT---TGCCGCTCACGTAGAAGT	533
Db	444	GlyProCysArgProAlaAlaThrGlyAlaProProProGlyCysAlaThrArgArg---	462
Qy	532	CGGCAACGCCACCGCGCTCTTGGGACAGGTACGAGCAAGCCCTGGTCGATGACGTTGT	473
Db	463	-----GlyHisAlaGly---GlyThrArgArgProArgGluSerGlyAla	476
Qy	472	GGAAACGGTGGAAATCATPCTGTAGCGAGTAGDAGAAGGTGATGAGCGTGCAGGTCCTCAG	413
Db	477	Gly-----	480
Qy	412	GGGGCGCAATTTGGCAAGCGTCGGCCTCCACGA-----CCTGGACATTTCTCCAGCCCT	359
Db	481	SerGlyArgThrGlyVal-----ProProAlaArgPheProGlyAlaSerAlaProArg	498


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Db 450 GlyProAlaThrSerLeuAlaasp---ProAlaArgProAlaAlaProArgArgArgLeu 468
Qy 628 CAATGTGTGTCGATGCGAAGATCGATCGCCAGAGAAACGGCGCAGACCATCTGCG 569
Db 469 ProAlaLeuProAlaThrArgAlaAlaProAla---GlyAlaGlyGlyGlnSerArg 487
Qy 568 GCAGGGGAGGTGCTACTTGGCGCTCAGCTGAAGTCCGCAAGTCCGACCGCCAGCGCGTCTT 509
Db 488 LeuGlyAlaGlyHisArg---ArgGlyProArgHisArgAlaArgProAlaArg--- 505
Qy 508 GGCACAGGTACGAGCAAGCGCTGTCGATCGATGCTGTGGAACGGTGGAAATCATCTCGTGAAG 449
Db 506 GlyThrGlyThrProPro-----SerAlaGlyTyProArgAlaAlaLeuArg 521
Qy 448 ACTAGAGAGGTGATGAGCTGCGGTGCTCAGGGGGCGCAATATGGCAAGCGTCGG 389
Db 522 AlaAlaArgArg-----ThrLeuArgAlaPro---GlyAlaMetAlaGlyGlyArgHis 538
Qy 388 CCTCCAGCACCTGGACATCTTCCAGCCCTTGGCCTTGGCCTTCTTCTTGGCCACTCGC 329
Db 539 -----GlyHisGlnHisProArgProAlaGlu-----ProValArg 551
Qy 328 ACAGCGAGTGGCACAGGT-----CGACCACGTAGATGGACTTGAACCTTCGCCA 281
Db 552 LeuValAlaGlyProGlyHisProLeuAlaArgProArg-----ThrPro 567
Qy 280 GGTGATGATTAATCAGCCATCATATCGACATTTCTCCCGCAGTGCACACCCAGGTCAACCC 221
Db 568 GlnArg-----ArgGlyMetArgGlyArgProGlyThrAlaArgArgGlyAlaPro 584
Qy 220 AGATGAGGTTCAGCGCTCGCCAGCGCGGCGAGCAAGCAGCGCTGGGGCCCGTGA 161
Db 585 GlyProGlyArgGlnProArgThrAlaGlyArgSerArgProArg-----ArgArg 601
Qy 160 AGCTTCCAGGCGACGAGCTGATCATCGC-----CCTTCTTGTGTCGCGA 116
Db 602 SerThrAlaGly-----ArgLeuHisArgLeuCysArgGlyAsnProArgAlaValGly 619
Qy 115 ACCATATGCGCGCAGAACGGTCAGGTATCTCTTCATCTGCTGC----- 74
Db 620 AlaThrAlaProGlyGlyArgProGlyGlnProGlyAlaAlaGluProAlaArgProArg 639
Qy 73 -----TGAGCTTGACCTTCTCAGGAGAAAGTTCTTCTTGTGTAGCTCG 29
Db 640 ArgArgProProGluLeuAlaAlaAlaLeuAlaGlyLysArgArgAlaAspAlaArgAsn 659
Qy 28 CAGGCGGCGCTCAGCACCGCCACCCCA 2
Db 660 AlaAlaGlyArgProAlaProAlaPro 668
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RESULT 6

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US-09-252-991A-17231
; Sequence 17231, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 17231
; LENGTH: 2294
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-17231
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Alignment Scores:

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Pred. No.: 1.97e-15 Length: 2294
Score: 324.00 Matches: 274
Percent Similarity: 29.3% Conservative: 43
Best Local Similarity: 25.3% Mismatches: 280
Query Match: 9.0% Indels: 485
DB: 2 Gaps: 58

US-10-620-914-44 (1-1947) x US-09-252-991A-17231 (1-2294)

Qy 20 GCCGCCCTGCGAGCTACACCAAGAGAACTTCTCCCTCG----- 58
Db 55 AlaGlyHisArgGlnArgProArgArgAlaAlaGlyTyrAlaValGlnHisProArg 74
Qy 59 ---AGAACTCAAGCTCAGCAGCA-----TGAAGGATG 88
Db 75 ArgArgSerGlyAlaGlyAlaAlaGluCysArgGlyLysProAlaArgTrpHisArgLeu 94
Qy 89 ACCTGACCGTTCGCGCCATATGTTGCGCAGCAAGAGGCGCATGATCAGCGTGCTC 148
Db 95 ProArgPro---AlaAlaGluAlaGlyArgHisProArgHisGly----- 108
Qy 149 GCCTGAGAGCTTCTACGGGCCCGCAGCGCTGCTTGTGCTGCCGCGCTGGC----- 200
Db 109 -----ArgGlyGlyArgGlyProArgArgArgProLeuArg-GlnProGlyAlaGlySe 126
Qy 201 -----CGAGCGCTCGAACCTCATCTGGTTCGCTGGTGGTGGTGGCCTG 244
Db 126 rAlaArgArgGlnCysArgLeuArgGluProArgProGlyGlyProGly----- 142
Qy 245 GGGAGATGTCGATATGATGCTGATCATCGACCTCGCGAAGTTCAAGTCCATCTACG 304
Db 143 -----GlnProGlyValProProAlaAspArgAl 152
Qy 305 TGGTGCACCT-----GTGCCACTCGCTGTCGAGG 334
Db 152 aArgArgProArgArgIleArgArgGlyArgArgAlaGlyProArgGluAlaArgG 172
Qy 335 T---GGCCAGAAAGCGCAAGGC-----CAAGGCTTGAAGAATGT----- 374
Db 172 yProGlyProGluProGlyArgGlyLeuProAlaAlaGlyAlaArgHisCysArgArgAl 192
Qy 375 -----CCAGTCTG----- 383
Db 192 aAlaProGlyValLeuArgGlnGlyAlaAlaGlyProAlaProAlaArgSerPr 212
Qy 384 -----GGAGCGCGACGCTTCCCAAT 403
Db 212 oArgArgAlaGlyGlyGlyIleGlnArgArgGlyArgLeuGlyAsnArgArgLeuProAl 232
Qy 404 TTGCGCCCCCTGAGGGCACCGCAGCTCATCCTTCTCTCTATCTC-----GC 451
Db 232 aAlaAlaThrGlyGlnProArgArgGlyProHisTrpSerProValProArgAlaProAl 252
Qy 452 TCAGATGATTCACCGCTTCCACAACTCATCGACCGCTTGTCTGCTGA----- 500
Db 252 aAlaProAlaGlyAlaValProArgThrGlyGlyProGlyArgArgValLeuTyLeuHi 272
Qy 501 -----CCTGTC-----CCAAGACCGCTGGTGGCGG 526
Db 272 sArgGlnProAlaAlaSerArgGlyValProGlyValGlnProArgArgProGly----- 290
Qy 527 TTGCGCGATCTTACGTGAGCGGCAAGTACGACCTGCCCTCGC----- 569
Db 291 ---ArgGlnLeuArgProGlyAspAlaArgProAlaProAlaGlyAspGlyAspArg 309
Qy 570 -----CCAGATGCCCTGGTGGCGCGTCTCTCTGGCGATCGATCT 610
Db 309 sArgGlnGlyAspArgHisProAspArgArgGluGlyLeuArgArgAlaArgAspAl 329
Qy 611 TCGACAT-----CGACCAACATTGACATCGGCC-----CGAGCGCC 646
Db 329 aGlnArgProGlnProAspArgGlnArgGlnLeuArgProGlyGlyAlaArgArgArgPr 349
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QY 647 GCGC-----CTACCTGGAGCAGAAAGCTGGAGCGCTGGGAGCAGA 688
DB 349 oArgArgGluProAlaArgAlaLeuProAlaAlaGlyGlnGly-----ArgLeuGlyGlyAl 368
QY 689 ACACCCA-----GGGTTT----- 701
DB 368 aHisProArgProGlyGlnProAlaThrAlaGlyTyrArgProAlaAlaAspAlaGlyGln 388
QY 702 -----GATCCCTTA-----CG 712
DB 388 yAlaAlaAlaAspProLeuProArgArgLeuHisLeuPheArgThrGlyProArgGlnArg 408
QY 713 TGCCTG-----CCTGGCGCCCTACTACGCTGGGATTTGGCGCTGCCCGCAGCTGGCC 769
DB 408 gAlaLeuGluAlaAlaAspAlaLeuArgArgLeuProHisArgArgProAlaPr 428
QY 770 ACGCCCTGCACGAGCGCTGGA-----GCGCGCCGCCTAT----- 806
DB 428 oArgAlaGluProGlyLeuLeuGlyHisSerArgIleSerAsnAspAlaSerHisArgAr 448
QY 807 -----GTTCCCGCCACCTTCCT-----GT 826
DB 448 gSerLeuArgHisProGlyArgArgGlnArgLysProAlaArgProHisHisAs 468
QY 827 ACAGCAGTCTGGGAGGACCCCGAGCGGATATGGA----- 863
DB 468 pHisAlaAlaSerArgArgProArgProGlyThrGlyArgArgProProArgArgArgSe 488
QY 864 -----GATGATGAGATCAACCCCAAGCACCGCTGCTGACCCCTGACTAGCG 910
DB 488 rLeuHisAlaAlaAlaAspGly---GlnPro-----GlyAlaAlaGluArgProAr 504
QY 911 GCGCTGCAATGCCCTGAACCTGCTGTGTCAGGGGGCGCGCAGGTGTGTCGTGGACT 970
DB 504 gArgArg-----ProGlnProAlaGlyAlaGlyArgArgPro---ThrAlaGlyAspAl 521
QY 971 GCACCCCGCCGAGTC-----GGCGCTTCGGAGCTGAAGAAGTGGCCATTGACGAGC 1024
DB 521 aHisProProAlaGlnHisHisArgProSerGlyAlaGlyGlnProAlaArgAlaThrAl 541
QY 1025 TGGAGTTTGAGGAGCTGTGGCAGCTGTTTCGGCGAGGGCGT---GCACCGCGCATTTGAGG 1081
DB 541 a-----ArgLeuProAlaProValArgGlyGluGlyThrProGlyArgArgGl 557
QY 1082 AGCTGTACGAGAAGAGCTGGCGCCCTTCCTGTGCAAAACAGCA----- 1127
DB 557 yAlaGlyArgSerAspAlaGlyAlaLeuArgAlaLeuHisArgProArgArgSerGlyAl 577
QY 1128 -----CAACTTCTGTCCAAGCG---CCTCTGTGTTACTTCCAGC 1162
DB 577 aGlnHisAlaValGlyGlnHisGlnArgLeuGlyGlnAlaGluProAlaAspHisProAl 597
QY 1163 ACGGCTGTACTACGAGCGCGCATTTGG----- 1190
DB 597 aGlnArgGlyLeuGlyArgArgGluGlyLeuProValAlaAlaArgThrLeuProAlaGluPr 617
QY 1191 -----CAAGCTGTGCTGGTGTGCTGAGTGCCT----- 1217
DB 617 oAlaProAlaProAlaProAlaGlyAlaAlaValProValHisGlnProArgLeuArgAr 637
QY 1218 -----GCGCGTGTGCTGGGAC 1234
DB 637 gProLeuProGlyHisAlaArgArgProGlnProThrGlyAlaAlaAlaArgAlaHisAr 657
QY 1235 TGGGCAAGACCGCTCAAGCGCTCGCCCAACGGCGCCCAATGGAGGAGCGCGCTCTGT 1294
DB 657 gGlyGlyAspProGlnHisProArgArgValArgAlaArgThrValAlaAlaLeuAlaAr 677
QY 1295 GGGACAGCAACATGCTCATCCA-----CTTCGTGA 1324
DB 677 gProGlnArgAspAlaArgProProPheAlaAlaProAlaAlaValGlyArgTyrArgHi 697
QY 1325 AGAAGCGGCCCAAGCGCTGGTGTGCTGTTCTGTTCAAGTT----- 1364

DB 697 sArgProGlyLeuAlaAlaGlyLeuAlaValArgProAlaAlaAspGluAlaGlyArgArgAr 717
QY 1365 -----CGTGA 1369
DB 717 gArgAlaGlyValGlnAlaHisProArgHisArgArgAspProGlyAlaGlyHisArgPr 737
QY 1370 GCCTGGTGTCTTCAACAAGGC-----CGTCTGTGGTTCCGCGCGC 1411
DB 737 oProGlyGlyAlaAlaAlaGlyAspArgAlaAlaThrProGlyAlaLeuProArgArgAr 757
QY 1412 GCGTGCCTGGCGCAACA-----GTACGGCGCTGATCAAGCGCGGACGCGATCC 1456
DB 757 gHisGlnGlyProAlaGlyGlyGlyArgArgProLeuGlyGlyArgHisPr 777
QY 1457 CCA----- 1459
DB 777 oArgArgArgAlaValArgGlnArgGlnArgAlaArgValProAlaAlaAl 797
QY 1460 -----TT 1461
DB 797 aAlaAlaHisArgArgArgProAlaGlnGlyGlnGlyProGlyAlaGlyHisArgAlaAl 817
QY 1462 GAGAACTACTATCGCGCACCATGGAGCGGCTGGCGGAGAACTCGCAGCTGC----- 1513
DB 817 eAlaThrThrGlyArgSerProArgCysAlaThrArgProThrGlyAsnCysProArgPr 837
QY 1514 -GCAAGCAGAACTACTTCTACTCAACTGCTCTACCGGCAAGTCTTCGCGGACAACTGC 1572
DB 837 oAlaProArgArgSerProThrSerAlaArgProProAlaThrProAlaAlaSerPr 857
QY 1573 CCCACCTACCTGCGCGAGG-----CGSCCTTCGCCCACTCAAGAGTGGCG- 1618
DB 857 oProGlyAlaAlaThrProSerArgTyrArgProMetProAlaProLysAlaAlaHi 877
QY 1619 -----TGGTGGACAACCT-----GACGCTCTCCACC 1644
DB 877 sAlaThrAlaGlyTyr-LysSerProTyrSerArgArgAlaArgAsnGluArgLeuProG 897
QY 1645 AACTTCTTCAT-----GGAGGAGCT----- 1664
DB 897 lnLeuLeuArgAlaLeuGlyGlyAlaGlyAlaArgProAlaArgProGluProAspHisL 917
QY 1664 ----- 1664
DB 917 euValProArgProAlaAlaAlaProGlyGlnLeuArgThrValGlyLeuGlyAspGlnP 937
QY 1665 -----CAAAGCGCGCAC 1677
DB 937 roLeuGlyAlaAspArgProAlaValProGlyLeuAspArgLeuProArgAlaAlaHis- 956
QY 1678 TACACCAAGGTGATCTGATGGACCACTGGCTGGTGGATATGCCCTGCGCCCAACGAG 1737
DB 957 --ArgAlaGlyProAlaGlnArgGlyGlyHisAlaGluSerArgArgGlyGlnArgA 976
QY 1738 CTGSCCGA-----CATCTGGCGCTCCGCTCCCTCAG----- 1745
DB 976 laGlyArgArgGlnArgArgHisArgArgArgAlaGlyAspProGlnAlaThrHisGlyA 996
QY 1746 -----GTGCTTGGCGCAGAGTTGCGCGCGCGGCATCGT----- 1781
DB 996 rGlyGlyProGlyProAlaGlnAlaGlyGlnAlaGlyArgGlnArgAlaAlaGlnProValA 1016
QY 1782 -----CATCTGGCGCTCCGCTCCCTCAG----- 1805
DB 1016 rgValAlaLeuValArgAspHisArgProAlaArgPheGlyGlnAspHisArgAlaAspG 1036
QY 1806 -----CCGCGCCCTA-----CGCCGAGCTCATCCAGAGGC- 1835
DB 1036 luLeuArgProGlyLeuProAlaArgArgThrAspGlyArgArgGlyAspProArgGlyA 1056
QY 1836 -----GGCCTTCGAGCTGCTGCATCCCGCGCCCACTCAGGCTACATGAC 1884

Db 1056 rgArgHisAlaGlnLeuArgLeuValValHis-----ArgArgSerGlyAlaAlaGlyH 1074
QY 1885 CGGTCAACATGTACAGCTCTTTCATGTGCGCCCGCGAAGGCGCCCAAGAGACAA 1943
Db 1074 IsArgArgPro-----LeuTyrHisProGlyGlnProArgProGlyGlyGln 1089
RESULT 7
US-09-252-991A-27068
; Sequence 27068, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 27068
; LENGTH: 638
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-27068

Alignment Scores:
Pred. No.: 1,39e-15 Length: 638
Score: 223.00 Matches: 194
Percent Similarity: 32.6% Conservative: 36
Best Local Similarity: 27.5% Mismatches: 239
Query Match: 8.9% Indels: 236
DB: 2 Gaps: 38

US-10-620-914-44 (1-1947) x US-09-252-991A-27068 (1-638)

QY 1939 CTTCTTGGCGCCCTTCGCGGGCCATGTAGAAGAGCTGTACATGTGTGACGGCTCCA 1880
Db 66 ProArgGlnArgArgArgAlaProAlaGlyArgAlaAlaSer-----Pro 81
QY 1879 TGTAGCCCTGAGTGGCGGGGGATGACGCGCAGCTCGCAAGCCCG----- 1835
Db 82 GlyLysProArg---ArgGlyLeuAlaGlyAlaThrAlaGlyProArgProArg 100
QY 1834 -----CCTTCTGGATCAGCTCGG-----GTAGGGCGGCTGAGGAGCGGAGCGCC 1787
Db 101 AlalysProArgGlyValAlaArgIleGlnArgArgProAlaArgArgGlnAla 120
QY 1786 AGATGACGATCGCGCCCGCAACCTCTTGGCCAGGC---ACTGCGCCAGCTCGTTGG 1730
Db 121 -----ArgArgProAlaGlyProAlaAlaThrGlyArgAlaArgProHisArgGln 138
QY 1729 CCACGGGCA----- 1721
Db 139 ProGlyThrMetValArgLeuProGlyArgArgGlyAlaAlaProGlyArgArgLeu 158
QY 1720 ---TATCCAGCCAGTCCACGTGGCTTCAGAAATCACCTTGTGTAGTGGCGGCTTGA 1664
Db 159 ProHisProAlaAlaAlaArgGlnProAlaProAspPro----- 171
QY 1663 GCTCCTCCATGAAGAAGTTGGTGGAGACGGTCAGGTTGTCCA-----CCACGCCAC 1613
Db 172 -----ProGlnProGlyProArgGln 178
QY 1612 TCTTGAAGGTGGCAAGCCCGCTCCGCGAGTAGGTGGGCGAGTTGTGCGCGAGGA--- 1556
Db 179 Ala---GlyLysArgGlnProGlyArgArgArgArgAlaArgIleGlyGln 197
QY 1555 ACTTCCGCTGAGCAGTTGTAGTAGAGTAGTCTGCTTGGCAGCGTGGCAGTCTCCG 1496
Db 198 ProAlaArgAlaGlyArgAlaAspArgGlyLeuAlaAlaAlaArgArgAla----- 214

QY 1495 CCACGCGCTCCATGTCGCGCGATGTAGTTCTCAATGGGATGCCGTCGCGCTTGTATCA 1436
Db 215 ---ArgArgAlaThrLeuGlyGlnArgArgLeuArg----- 225
QY 1435 GCGGTACTGCTTCCCGCGCAGCGCGCGCGAACCACAGCACGCGCTTGTGAAGACA 1376
Db 226 ---ArgHisAspGlyAlaGlyArgArgArgGlyTTPArgArgGlnCnArgArgPro 244
QY 1375 CCAGGCTCACGAACCTTGACGAACACACACAGCGGCTTGGGCGCTTCTTCAGAAAT 1316
Db 245 ArgArgGlyAlaAlaAlaArgThrArgGlnProAlaAla---ThrLeuSerGlyArg--- 262
QY 1315 GGATGAGCATGTCGTCCACAGACGCGCTCTCTCCATTTGTGGGCGGTTGGCGA 1256
Db 262 ----- 262
QY 1255 GCGCTTGACGGTCTTCCCGAGTCCACAGCACGCGCGCAGGCACTGCAGCACCCAGACA 1196
Db 263 -----ValAlaProHisProArgProAspArgAlaSerProAlaThr 276
QY 1195 GCTTGGCCCATCGCGCTGTAGTACAGGCGCTGTGAAGTACCAGAGGCGCTTGGACC 1136
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QY 1135 AGAAGTTGTGGCTGTTTGCACAGGAAGGCGCAGCTTCTTCTGTACAGCTCTCTCAA 1076
Db 288 -----AlaProGlyProGlyHis-----ProGly 295
QY 1075 TGCGGGTGTCACGCCCTCGCGCAACAGCTGCCACAGCTCTCAAACTCCAGCTGCTCAA 1016
Db 296 ThrAlaGlyAlaArg---ArgThrProAlaProAlaArgProGlyThrProAspProGly 314
QY 1015 TGGCCACCTCTTCAGCTCCAGAAAGCGCCDAGTGGCGGGTTGCGAGTCCACCCAGACCA 956
Db 315 TrpAspArgProAspPro---AlaHisArgProArgHisArgGlnProAlaAlaThr 333
QY 955 CCTGCGCGCGCCCTGCAACAGAGTTTCAGGCAATTCGACG---CGCGCTAGTTCAGGG 899
Db 334 ProGlyAlaGlyProArgAlaThrGlyAlaGlyAlaLeuGlyLeuGlyArgArgArgLeu 353
QY 898 TCAGCAGCTGTCCTTGGGTTGATCTCCATCAGCTCCATATCGGCTCGGCGCTCTCC 839
Db 354 LeuAlaPro-----HisIleProAlaTyrProHisArgGlyPro--- 366
QY 838 ACAGCTGCTGTACAGAAAGTGGCGGCAACATGGCGCGCTCCACGCGCTCTCGT 779
Db 367 -----AlaGlnProGlyArgPheAlaGluProProAlaGlnLeuProArg-----Arg 382
QY 778 GCAGGGCGT-----GGCAACGCTGGGAGGCGGCAATCC 743
Db 383 AlaGlyArgArgAspProProArgArgThrGlyArgArg-----GlnGlnPro 399
QY 742 ACAGTAGTAGGCGCGCAGCCACGCGCAGTAGGGATCGAACCTCGGTGTTCTGCT 683
Db 400 AspProGlyArgGlyGlnArgProAlaArgArgGlyArgAlaProGly-----Arg 417
QY 682 CCCACAGCGCTCCAGCTTCTGCTCCAGGTAGGCGCGCTCGGGGCGGATGTCAATGT 623
Db 418 ArgTyrArgAlaAspProArgArgProArgArgHisGlySerGlyAsp-----ProAla 435
QY 622 TGTGATGTGGAAGATCGATCGCAGAAAGAACCGCGCGACCCAGGCGCATCTGGCGCAGG 563
Db 436 GlyArgArgArgGlnProAspArgArgGlnSerGlnArgArgProGlySerGly 455
QY 562 GCA-----GGTCTACTTCCCGCTCA-----CGTAGA 536
Db 456 AlaTrpProAlaGlyAspArgArgGluProGlyArgProAlaArgAlaGlyArgArgGly 475
QY 535 AGTCGCAACGCCCAACCGCGCTTGGGACAGGTACGAGCAAGCTGTGTCGATGACGT 476
Db 476 AlaArgGlnArgProValAspArg-----AlaProGlyArg----- 487

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QY 475 TGTGAAACGGTGAATCATCTGTAGCGAGTAGGAGAGGTGATGAGCGTCCGGTGCCT 416
Db 487 -----
QY 415 CAGGGGGCGCAATTTGGCAAGCGTGGCGCTCCACGACCTGGACATCTTCCAGCCCTTGG 356
Db 488 -----GlyValGlyAspHisArg-----
QY 355 CCTTCGCCCTTCTTGTGGCCACCTCGCACAGCGAGTGCCACAGGTGCGACCACTAGATGG 296
Db 494 -----GlnArgAlaAspGlyAspProLeuAspArg-----
QY 295 ACTTGAACCTCCGACAGGTGATGTAATCAGCCATCATATGACATCTCCCGAGTGGCCAC 236
Db 504 -----ArgThrAspGlnProAla-----
QY 235 CACCCAGGTCAACCCAGATGAGTTGAGCGCTCGGCCAGCGGGCAG---CAAAGGCGAG 179
Db 515 HisArgGlyArgProArg-----ArgArgProGlyProArgLeuArgArgGly 530
QY 178 CGGCTGGGGCCGTAGAACTCTCCAGCGAGCAGCGTATCATCGC----- 131
Db 531 ArgArgGlySerProLeuAlaGlyProAlaHisArgArgHisArgGlyAspProAla 550
QY 130 -----CCTCTCTGCTGCGCAACCATATATGCGCAGAACGGTCAAGTCACTCT 83
Db 551 AlaHisArgProProAlaThrGlyArgAlaAlaGlyGlyHisAlaGlnProGly 570
QY 82 TCATGCTGCTGAGCTTGAGCTTCTCCAGGGAGAAAGTTCTTCTGTGTGATCGCGAGCC 23
Db 571 ArgAlaCysArgThrHisArgArgThrGlyArgArgGlyGlyArgAlaGlyArgSer 590
QY 22 GCGCTCAAGACCCG 8
Db 591 GlyArgArgAspPro 595

RESULT 8
US-09-252-991A-18296
; Sequence 18296, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252.991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 18296
; LENGTH: 467
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-18296

Alignment Scores:
Pred. No.: 3.14e-15 Length: 467
Score: 317.50 Matches: 178
Percent Similarity: 32.7% Conservative: 26
Best Local Similarity: 28.5% Mismatches: 198
Query Match: 8.8% Indels: 222
DB: 2 Gaps: 34

US-10-620-914-44 (1-1947) x US-09-252-991A-18296 (1-467)
QY 1828 GGATCAGTTCGGCTAGCGGGCTGAGGAGGGAGCGGCAGATGACGATCGCGCCG 1769
Db 3 GlyCysAlaGlyCysProAlaGlyCysGlyArgArgGly----- 15
QY 1768 GCGCAACCTGCTTGGCCAGGCACTCGGCGAGTCTGTTGGCCACGCGGCATATCCAGCCAGT 1709

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Db 16 -----AsnTrpProProAlaArgAlaGlyPheProProPro-----ProAlaCys 31
QY 1708 CCAGCTGGTTCATCAGAATCACCTTGGTGTAGTGGCGCTTTGAGCTCTCCATGAAGA 1649
Db 32 ArgProGlyThrGlySerSerArgTrpAsnArgAlaGly----- 44
QY 1648 AGTTGGTGGAGACGGTCAGGTTGTCCACACCGCCACTCTTGTAGGGTGGCGAAGGCCGCT 1589
Db 45 -----ArgAlaArgGlyCysPro-----GlyCysAlaAlaProPro 56
QY 1588 CGC-----GCAGGTAGTGGGGCGAGTGTGCGCAGGAACCTTCCGGTGGAGGC 1541
Db 57 AlaGlyValProGlyAlaGlyArg-----SerValProAlaProAlaCysArg----- 72
QY 1540 AGTTGTAGTAGAAGTAGTTCTGTCGCGACGTCCGAGTCTCCGCCACCGCGTCCATGG 1481
Db 73 -----ArgArgArgHisArgArgSerArgProSer-----GlyArgProArg 88
QY 1480 TGGCGCGATGTAGTCTCAATGGGATCGCTCGCTTGTATCAGCGCGTACTGCTTGC 1421
Db 89 GlnGlyArgArgGlySer-----ProThrAlaAlaLeuArgLeuArg 102
QY 1420 CCGCGACCGCCCGCCGAACCCACAGCAGCGCTTGTGTAAGAGAGCACCGAGGTCTCAACT 1361
Db 103 ProAlaArgArgArg-----ArgHisPro----- 111
QY 1360 TGACGAACAGCCACACCGCGCTTGGCCCGTCTTTCACGAAGTGTGATGACATGTTC 1301
Db 112 -----AlaTrpArgArgArgSerAlaSerArgProAla----- 122
QY 1300 TGTCCACAGACGGCTGCTCTCCATTTGTGGCGGTGGCGAGGCGTTGACGGTCT 1241
Db 123 -----GlyAlaProPro----- 127
QY 1240 TGCCAGTCCAGCACCGCCAGGCACCTGACACCCAGC----- 1199
Db 128 AlaProCysProAlaProArg--GlyAlaGlyAlaProSerValArgGluArgProAla 146
QY 1198 ---ACAGTTGCCATGCCGCCCTGGT-----AGTACAGGC 1166
Db 147 GlySerAlaProProProArgProAlaArgArgProProAlaProHisArgThrGly 166
QY 1165 CGTCTGGAAGTACAGAGGCGCTTGGACCAAGATTGTGGCTGTGTTGCGACAGGAAG 1106
Db 167 GlySerGly-----TrpArgArgArgGly-----ArgThrArg 178
QY 1105 GCGCAGCTTCTTCTCGT-----ACAGCTCTCAATGCGCGGTGCACGC 1061
Db 179 ArgProAlaAlaSerArgArgProAlaGlyProAlaGlyArgProGlyGlySerArg 198
QY 1060 CCTGCGCAACAGCTGCCACAGCTCCTCAACTCCAGTGTGTAATGCCACCTTCTTCA 1001
Db 199 AsnArgArgArgAla----- 203
QY 1000 GCTCCAGAAGCGCGACTGTCGCGGGTTGACGTCACCGACACCCACTTGGCGGCCCT 941
Db 204 -----GlyCysArgProAlaArgProValAlaArgAla 215
QY 940 GCACCAAGAGTTTCAGGCAATTGACGCGCGCTAGTCAGGGTCAGCACCGTGTCTTGG 881
Db 216 GlyPro--GlyProGlyArgCysArgArgArgCysAlaTrpSerProCysPro-- 233
QY 880 GTTGATCTCCATCACCTCCATATCCGGCTCGGGGTCTCCACGACTCGTGTGTACAGA 821
Db 233 ----- 233
QY 820 AGGTGGCGGGAACATAGGGCGCGCTCCACGCGTCTCGTGCAGGGCGTGGCCAAGC 761
Db 234 -----ThrProArg--AspArgAlaGlyAlaGlyAspArg 244
QY 760 TGGGACGCGGCCAATCCACAGTGTAGTAGGGG-----CGCGACGACCGCAGCT 710

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Db 245 HisValProAlaGlyAspAlaArgAlaAlaGlyTyrProThrGlySerArgCysAlaArg 264
QY 709 AGGGGATCGAACCCCTGGGTCTCTGCTCCACACACGCGCTCCAGCTTCTGCTCCAGTAGG 650
Db 265 ArgSerGlySerAlaGlyCysAlaArgPro-----ProArgSerCysValArg 281
QY 649 CGCGCGCTCGGGCGGATGTCATGTTGTCGATGTCGAAGTCAAGATCGATCCGCAAGAACA 590
Db 282 TrpAlaAlaArg-----ArgValAlaArgAspSerAlaArgArgSer 295
QY 589 GCGCGACACAGGGCATCTGGCGCAGCGGCGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTG 530
Db 296 AspArgProValArgSerAlaLeuArgGlyLeuProAlaAlaArgArgSerArgProArg 315
QY 529 CAACGCCACACAGCGCTTGGGACAGGTACGACCAAGCTGTCGATGACGTTGTGGA 470
Db 316 HisArgArgProGlySer-ValProProValArgThrSerArgAla-----ThrProAr 333
QY 469 ACGTGGGAATCATCTG-----GAGCGAGTAGGAGAGGTGATGACGCTCG 425
Db 333 GArgTrpHisAlaArgTrpGlnAlaAlaAlaArgArgProGly-SerValLeuSerSerA 353
QY 424 CGGTGCTCTCA-----GGGGCGCAAAATTGGCAAGCGTGGCGCTCCACGA 380
Db 353 laThrProAlaAlaProGlyValArgGlyTyrProArgGluTyrAla-ArgAlaProArg 372
QY 379 CTTGACATCTTCCAGCCCT-----TGGCCTTGGCCTTCTTCTTGGCCA 335
Db 373 ProAlaLeuProGlyArgProAlaAlaAlaArgProAlaArgProArgProCysArgArgPro 392
QY 334 CTTGCCACAGGAGTGGCACAGGTGACCA-----CGTAGATGGACT 293
Db 393 AlaAspArgSerProGlyGlnGlyArgProProGlySerSerAlaThrArgArgTrpArg 412
QY 292 TGAATCTGCCAGGTCGATGTAATCAGCCATCATACGATTCCTCCCGAGTCCACAC 233
Db 413 -----ProCysHisArg 416
QY 232 CCAGGTCAACCCAGATAGGTTCCAGCGCTCGGCCAGGC-----GGGCAG 188
Db 417 ArgAlaGluProAlaAlaAlaProAlaAlaGlyTyrProGlyAlaAlaAlaArgSerAlaThr 436
QY 187 CAAGGCGAGCGCTGGGGCCGTGAGAGC---TCTCAGGCGGACGACGTCATCATCGC 131
Db 437 ArgArgThrHisAlaGlyArgArgGlySerAlaThrProSerGlyArgArgAspArg 456
QY 130 CTTTCT 125
Db 457 ProAla 458

RESULT 9
US-09-252-991A-31760
; Sequence 31760, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 31760
; LENGTH: 1706
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-31760

Alignment Scores:

Pred. No.: 6.27e-15 Length: 1706
Score: 316.50 Matches: 193
Percent Similarity: 33.1% Conservative: 44
Best Local Similarity: 26.9% Mismatches: 249
Query Match: 8.7% Indels: 231
DB: 2 Gaps: 36
US-10-620-914-44 (1-1947) x US-09-252-991A-31760 (1-1706)
QY 1846 CGTGAAGCCCGCTTCTGATCAGCTCGGCGGTAGGCGGCTGAGGAGCGGAGCGCC 1787
Db 276 ArgArgGlnProAlaGlyAlaThrAlaAlaGlyLeuArgHisArgProGly---HisProAla 294
QY 1786 AGATGACGATCGCGCGCGCCGACCTCTGTTGGCCAGCACTCGGCGCAGCTGTTGGCCA 1727
Db 295 ArgLeuArgArgGlnProAlaArgLeuArgSerGlyGluArgProAlaGluSerPro 314
QY 1726 CGGCGATATCCAGCCAGCTCCACGTGGT----- 1700
Db 315 ArgArgThrProGlyGluLeuArgGlyArgArgProAspAlaLeuProArgLeuAlaGly 334
QY 1699 ---CCATCAGAATCACCT-----TGGTGTAGTGGCGGCTTTGAGCTCCT---CCATGA 1652
Db 335 LysProGlyArgTyrProAlaGluPheAlaArgGlyAlaAlaProAlaProGlyPro--- 353
QY 1651 AGAAGTTGGTGAGACGGTTCAGGTTGTCACCCACCTCTTGGAGG-----TGG 1601
Db 354 -----LeuAlaAlaAlaValProArgArgHisAlaAlaArgAlaAlaGluProTrp 369
QY 1600 CGAAGCGCGCTCGCGCAGGTAGTGGGCGAGTGTCCGCGAGGACCTTGGCGGTGAGGC 1541
Db 370 ArgArgProAlaGlyGlyArg-----AlaAspArgThrAlaThr----- 383
QY 1540 AGTTGTAGTAGAAGTAGTTCTGCTTGGCAGCTGCGAGTCTTCCGCCACGCGCTCCATGG 1481
Db 384 AlaProAlaArgProArgThrAlaCysAlaAlaAlaValAlaGlyProArgHis----- 401
QY 1480 TGCSCGCGATGATTTCTCAATGGGATGCGCTCGCCTTGATCAGCGCGTACTGCTTGC 1421
Db 401 ----- 401
QY 1420 CCGCAGCGCGCGCCGACCCAGCAGCAGCGCTTGTGAAGAGCAGCAGGCTCAGCA--- 1364
Db 402 ---AlaArgGluGlnProArgThrLeuProGlyProArgProProGlyAlaAlaGly 420
QY 1363 -----ACTTGACGAACAGCCACACAGCGGCTTGGCGCGCTTCTTCCAGCA 1319
Db 421 ThrHisLeuAlaGlySerAlaGlnProAlaAlaProAlaAla---AlaArgProPro--- 438
QY 1318 AGTGGATGAGCATGTTGCTGCCACAGCGCGCTGCTCTCCATTTGCGCGCGTGG 1259
Db 439 -----AlaAlaLeuProAlaAlaArgAlaArg--- 446
QY 1258 CGAGCGCTTACCGCTTGTGCCAGTCCAGCACA-----CGGCCAGGCACTCA 1208
Db 447 ArgGlyArgArgGlnProProGlyArgProArgArgLeuArgProGly---Ala 465
QY 1207 GCACCCAGCAGCTTGCCTCCATGCCCGCTGGTAGTACAGCGCGCTGGAAGTACCAGA 1148
Db 466 ProValAlaAlaAlaPro-----AlaThrGlyGlyAlaAlaThrGluPro 481
QY 1147 GCGCGTTGGACAGAGTGTGGCTGGTTTTCGACAGAGAGGCGGCCAGCTTCTTCTCGT 1088
Db 482 GlyAla-----GlyAspSerArgHisArgCysArg 491
QY 1087 ACAGCTCTCAATCGCGGGTGCAGCGCTCGCGAAGCAGCTGCCACAGCTCTCAACT 1028
Db 492 SerGlyThrAspArgProGly---ArgProArgGlnProAlaAlaAlaArgAspProGly 510
QY 1027 CCAGCTGCTGAATGCCACCTTCTTACGCTCCAGAGCGCGCAGCTGCGCGGGTTCAGT 968
Db 511 ProGlySer---TrpProGlyProSerAlaAlaAlaArgAlaAlaArgArgGly---Asp 528


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QY 967 CCA-----CCGACA 959
Db 529 ProHisArgArgGluThrAlaLeuArgSerAlaAlaArgArgProArgArgAlaAsp 548
QY 958 CCACCTGGCGCGCCCTTCACACAGCAGGTTTCAGGGCATTGCAGCGCGCTAGTCAGG 899
Db 549 ProProGlyArgThrProAlaGlnProGlyGlnThrGluGlyAlaArg- 565
QY 998 TCAGCACGCTCTCTGGGGTTGATCTCCATCACCCTCATATCCGGCTCGGGGCTCTCCC 839
Db 565 ----- 565
QY 838 ACGACTGCTGTACAGGAAGTGGCGGAACATGGCGCGCTCCACGCGCTCTCGT 779
Db 566 -----LeuAlaArgArgThrAlaGlyThr-----AlaAlaProArg 578
QY 778 GCAGGGCGTGGCCAAACGCTGGCGAGCGGCCAATCCACAGTAGTAGGGCGCGCGACCC 719
Db 579 HisArgArgGlnProGluGlnProAlaGlyProArgProProAlaArgGlyAlaThrAla 598
QY 718 ACGCACGT-----AGGGATCGAACCTGGG 692
Db 599 ThrSerArgLeuProAlaLeuProTrpProArgArgProAlaArgSerHisArgProGly 618
QY 691 TGTTCGTCTCCACACGCGCTCCAGCTTCCTCCAGTAGCGCGGCTCGGGCGGA 632
Db 619 IleProGlyProAla--AlaProAlaProGlyThrThrArgArgAspSerArgArg 637
QY 631 TGTCAATGTTCTGATGTCGAAGATCGATCGCCAGAGAAACGGCGCGCACCGGCA--- 575
Db 638 -----ThrArgSerHisGlyAlaProHisAlaGln 647
QY 574 -----TGTGGCGGAGGGAGGTGCTTCTGCGCTCACGTAGTAGTGGCAAGC--- 524
Db 648 ProArgSerAlaAlaGlyLeuGluAlaAlaProGlyThrArgGlnSerGlyThrAlaVal 667
QY 523 CCACGAGCGCTCTTGGACAGGTACGAGCAAGCTGCTGCATGACGTTGTGGAACGGT 464
Db 668 GlnProGlyArgSerGlnGlyGlnArgGlnProArgArgSerArgGlyAlaAspAla 687
QY 463 GAATCATCGTGGCGAGTGGAGAGGTGATGAGCGTCGCGTGCCCT---CAGGGGCG 407
Db 688 ArgAlaGluProArgThrAlaArgGlnGlyHisArgArgAlaProGlyGlnProGln 707
QY 406 CAATTTGGCAGCGTGGCGCTTCCAGCCTCGACATTCTTCCAGCCTTGGCCCTTCGCT 347
Db 708 AlaMetGlyArgArgHisProPro-----AspArgGln 718
QY 346 TCTTCTTGGCCACTCGCACAGCAGTGGCAGAGTCGACAGTCGACCACGTAGATGGACT 287
Db 719 AlaLeuAlaAlaProAlaArgValHisArgAlaGlyArgArgThrArgProAspGluPro 738
QY 286 TCGCCAGGTGATGTAATCAGCCATCATATCAGCATTTCTCCAGTGCACACCCAGGT 227
Db 739 AlaProGlyLeuAlaAspGluPro-----ArgProGly 749
QY 226 CAACCCAGATGAGTTCAGCGCTCGGCA----- 197
Db 750 GlnProArgAlaAlaAlaGlnGlyArgAlaValArgHisGlyAspLeuArgArgSerLeu 769
QY 196 -----GGCGGCGAG 188
Db 770 AlaAspAlaGlyGlyValArgProAlaAspProLeuSerArgAlaGlyHisGlyGlyGln 789
QY 187 CAAGG-----CAGCGGCTTGGGCGCCGTAGA 161
Db 790 ArgArgArgGluAlaAspAlaAlaAspArgValLeuLeuGlnProArgGlyLeuArg 809
QY 160 AGCTTCCAGCGCAGCAGCTGATCATCGCTTCTTCTGCTCCGACACCATATGGCGCA 101
Db 810 GlyArgThrValArgArgSerAlaArgArgGlyArgArg------GlyAla 826
QY 100 GAACGGTCA-----GGTCATCTTTCATGCTGCTGAGCTTCTGAGCTTCTCCAGGAGAGT 47
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Db 827 AlaArgSerLeuArgGlyHisLeuGluProProArgAspGlnGlyLeuProGlyProPro 846
QY 46 TCTTCTTGGTGTAGCTCGAGCGCGCGGTAC-----GACCGACCCCA 2
Db 847 AlaThrGlyAlaGlnArgProAlaGlnHisHisProAlaAspProLeuPro 863
RESULT 10
US-09-252-991A-27341
; Sequence 27341, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 27341
; LENGTH: 1073
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (803)
; OTHER INFORMATION: Identity of amino acid at the above locations are unknown.
US-09-252-991A-27341
Alignment Scores:
Pred. No.: 1,58e-14 Length: 1073
Score: 310.00 Matches: 243
Percent Similarity: 28.1% Conservative: 41
Best Local Similarity: 24.0% Mismatches: 288
Query Match: 8.6% Indels: 440
Db: 2 Gaps: 47
US-10-620-914-44 (1-1947) x US-09-252-991A-27341 (1-1073)
QY 18 CGCGCGGCTCGAGCTACAC-----CAAGAAGAACTTCTCCCTGGAGAGCTCAA 68
Db 92 ArgCysSerCysThrLeuGlyAlaSerIleArgGluGluArgGlnProAspGluArgLys 111
QY 69 GCTCAGCAGCATGAAGGATGACCTGACCGTTCTTCGCCCATATGTTGTTCCGCGACGAGAA 128
Db 112 AsnAlaArgHis-----ValProArgArg 120
QY 129 GGGCGATGATCACGCTGCTCGCTGGAGAGCTTCTACGGGCCCCAGCGCGCTGCTTTC 188
Db 121 ArgArgProGlyProCysArgProGlyProLeuHisAlaArgLeuProArgValArgArg 140
QY 189 TGCCGCGCTGGCGGCGCTCGAACCTCATCTGGGTTGACCTGCTGGTGTGGCTGGGGA 248
Db 141 ProProArgGlnArgLeuAlaGlu----- 148
QY 249 GAATGTCGATATGATGGCTGATTACATCAGCTCGCGAAGTTCAGTCCATCAGTGGT 308
Db 149 -----HisArgArgArgArgArgLeuTyLeuArgHis 160
QY 309 CGACCTGTGCCACTCGCTGCTCGAGGTGGCCAGAA----- 344
Db 161 ArgArgGlnProLeuProArgArgGlyGlyHisValValHisGlnHisArgProGly 180
QY 345 -----GAAGCGAAGGCTGGAAGTTCAGGCT----- 380
Db 181 AlaArgGlyAsnGlySerHisArgGlyArgAlaAspProProAlaGlyLeuPheGlnSer 200
QY 381 -----CGTGGAGGC 389
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Db 201 LeuLeuArgHisGlyGlnProAlaArgHisArgThrLeuProGlnAlaArgAlaGly 220
QY 390 CGACCTTGCCCAATTTGCGCCCC-----TGAGGG 419
Db 221 ProArgPro-----ArgProArgValProHisHisArgArgPheHisArgGly 238
QY 420 CACCGCGAGCTCATCACCCTTCTCTA----- 446
Db 239 HisArgAspProProHisAlaLeuLeuProGluLeuProArgGlnAlaArgGlnGluAla 258
QY 447 CTCGCTCAGATGATTCACCGCTTCCA----- 473
Db 259 ArgHisHisAlaAspGlnArgLeuProArgLeuAspLeuProArgHisValAlaGlyArg 278
QY 474 CAACGCTCATCGACCA----- 488
Db 279 GlnGluArgArgProAlaGlyArgValArgLeuProArgAlaHisProProCys 298
QY 489 ---GGCTTGCTGCTACCT-----GTCCCAAGCGGCT 518
Db 299 LeuSerLeuLeuLeuProArgSerGlyArgSerGlyArgGlyArgValProArgTrpPro 318
QY 519 GGTGGCGCTGCGGACTT----- 536
Db 319 GlyGlyGlyValArgThrGlnAspProArgThrGlyArgArgProGlyGlyGlyValHis 338
QY 537 -----CTAGCTGAGCGGCAAGTACGACCTGCGCCCTCGCCA 572
Db 339 LeuArgAlaGlyValArgLeuArgArgArgArgProAlaArgGlyLeuProAla 358
QY 573 GATGCCCTGGTGGCGCGTTCTT---CTGGGATCGATCTTCGACATCGACAATTGA 629
Db 359 AspValGlySerValProAlaLeuArgAlaValHisLeuArgArgSerGlyAspLeu 378
QY 630 CATGGGCCCGGAGCCCG----- 647
Db 379 LeuArgProProArgProLeuLeuArgGlnProGlyGlyValArgArgThrAlaGlyHis 398
QY 648 -----CGCTTACCTGGAGCA----- 662
Db 399 HisProHisArgGlnGlyProHisLeuArgLeuProAlaAlaGlyArgValHisLeuLeu 418
QY 662 ----- 662
Db 419 ProAlaHisLeuGlyAspArgAlaGlyGlnGlyProLeuLeuGlnProTrpPhe 438
QY 663 -----GAAGCTGGACCGCTGGGAGCAGACACCCAGGGTTCATCCC 707
Db 439 HisLeuLeuArgProProGlyGlyLeuArgGlyGlyAlaGluHisArgAspHisArg 458
QY 708 CTACGTGCGTGGCT-----GCGCGCCCTACTACGTGTGGATTGGCCG 752
Db 459 AlaArgGlyLeuAlaArgProArgArgArgGlyArgProLeuLeuArg-----GlyAla 476
QY 753 CTTGCCAGCGTTGGCCACGCCCTGCA----- 779
Db 477 ProAlaLysSer---ProArgProAlaHisArgArgArgAlaArgAspAlaLeuHis 495
QY 780 -----CGAGGAGCGGTGGAGCGGCCGCCCATCTGTTCCGCC 815
Db 496 GlyLeuCysArgValArgArgGlnGlyGlnGlyAlaValSerGlyLysArgProGlu 515
QY 816 CACCTTCTGTACAGCAGTCTGGGAGGACCCGAGCGGGATAT-----GGA 863
Db 516 HisArgArgVal-----GlyProProAlaGlyAlaGluAlaArgProAla 530
QY 864 GGTGATGAGATCAACCCCAAGGACAC-----GGTGTGACCTGACTAGCGCGG 914
Db 531 GlySerSerAspArgProProGluArgAspValAlaAlaAlaAspProHisProArgThr 550
QY 915 CTGCATCCCTGAACCTGCTGGTCAGGGCGGCCGAGGTGTGTGGTGGACTGCA 974
Db 551 GlyArgTyrArgGlyProGlyAlaAlaArgGluHisArgGlyAsnArgGlyGlySerCys 570

QY 975 CCCCGCGCAGTCGGCGCTTCT---GGAGCTGAAGAAGGTGGCCATTTCAGCAGCTGGAGTT 1031
Db 571 ProArgArgSerProValSerAlaGlyAlaProProAlaProHisProAsnIleGlnGlu 590
QY 1032 TGAGGACGTGTGGCAGCTGTTGGCGAGGdGTCACCCGCGCATTTGAGGAGCTGTACGA 1091
Db 591 AsnProAsnGlyArgGlnGlnGlnGlyProAlaValAlaArgCysGlyAlaLeuHis 610
QY 1092 GAAGAAGCTGGCGCCTTCTGTGCGAAACACGACCACAACTTCTGGTCCAAGCGCTCTG 1151
Db 611 GlyLeuGlyAspAlaLeuHisGlyProAspArgProGlyPheLeuProArgSer----- 628
QY 1152 GTACTTCCAGCAGCGCTGTACTACAGGGCGCATGGCAAGCTGTCTGGTCTGCA 1211
Db 629 -----ValGluProValLeuValAlaLeuArgAla-----GlyProAla 641
QY 1212 GTGCTGCGCCGTGCT-----CCTGGGACTGGCGAGACCGTCNA----- 1250
Db 642 ValProAlaAspGlyHisAspAspLeuArgAlaGlyHisArgLeuProArgGlnArgArg 661
QY 1251 -----GCGCCTCGCCCAACGCGCCCAATGAGGAGCAGCGCGCTCTGTG 1295
Db 662 ArgLeuProLeuGlyAlaGlnArgLeuArgLeuProLeuGlyGly-----ProGlyVal 679
QY 1296 -----GGACAGCAACATGCT-----CATCCACTTCTGTGAA 1325
Db 680 MetAspValLeuGlyGlnArgThrValAspAlaPheGlyLeuHisProValArgGln 699
QY 1326 GAA-----CGGCCCCAGCCGCTGGTGGCTGTTCGTCAGTT 1364
Db 700 HisAlaArgArgLeuLeuPheProArgAlaGluProLeuGly---GlnAspArgHisArg 718
QY 1365 CGTGAGCCTGTGCT-----CTTCAACAAGCCCGTCT----- 1397
Db 719 HisSerProGlyAlaAlaHisArgGlyValGlnArgGlyArgAlaAlaProGlyGlnVal 738
QY 1398 GTGTTGCGCGCGCTGCGGCAAGCATAGC---GCTGATCAAGGCGGAGCGCAT 1454
Db 739 AlaAlaGluProArgArgAlaAlaGlnAlaAlaArgGlyAlaArgProGlyArgArgArg 758
QY 1455 CCC-----CATTGAGAACTACATCGCGG 1478
Db 759 ProAlaLeuArgLeuGluProTrpLeuArgGlnArgLeuGlnProGlyLeuHisArgPro 778
QY 1479 -----CACCATGGACGGCT 1493
Db 779 ValLeuAlaGlyProAspGlyArgAlaGlySerAspGlyLeuTrpHisGlyAspArg 798
QY 1494 GCGGAGAACTCGCACCGTGGCGCAAGCAGAACTACTTCTACTACAACCTCCCTCACCGCAA 1553
Db 799 AlaGlyLeuLeu***-----ArgArg 805
QY 1554 GTTCTGCGCGCAACTGCCCCCCTACTCTGCGGAGGCGG----- 1595
Db 806 GlyTyrAlaGlnArgAlaProArgHisProAlaArgGlyGlyAspLeuArgAlaAspArg 825
QY 1596 -----CTTCGCGCACCTCAAGAG---TGGCGTGGT---GGACAACCTGAC 1634
Db 826 ArgArgLeuGlnHisLeuArgHisProArgArgAlaGlyArgGlyThrGlyArgGlyAsn 845
QY 1635 CGTCTCCAC----- 1643
Db 846 ArgArgHisProAspLeuArgProTrpLeuGlnHisLeuArgProArgArgArgArg 865
QY 1644 -----CAACTCTTCATGGAGGACT 1664
Db 866 ArgAspAlaArgArgProGlyArgArgLeuArgProValHisProLeuHisGlnHisGly 885
QY 1665 CAAAGCGCGCACCTACACCAA-----GTTGATTCTGATGGACACAGTGGACTG 1712
Db 886 HisLeuGluHisGlyHisGlnProCysArgGlyGlySerGlyGlnGlyArgArgAlaAla 905

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QY 1713 GCTGATATGCCGTGGCCACAGAGCTGGCCGAGTGCCT-----GGCCAAGCAGGT 1763
Db 906 GlyAlaValArgArgGlyProPheAlaProArgHisAlaAspArgLeuGlyAlaGly 925
QY 1764 TGCCTGGCGGCGCATCGT-----
Db 926 LeuGlyGlyGluHisArgProAlaAlaLeuArgProGlyGlyAlaHisCysArgGly 945
QY 1782 -----CATCTGGCGCTCGGCTCCCT 1802
Db 946 ThrValLeuAspProAlaValAspLeuArgHisGlyPheHisAspAlaLeuCysAlaAsp 965
QY 1803 CAGCCCGCCCTACGCGAGCTGATCCAGAA----- 1832
Db 966 ValProGlyLeuArgProProAlaProArgProAlaSerThrAlaLeuProAspAla 985
QY 1833 -----GGCGGGCTTCGACGTGCGCTG----- 1853
Db 986 AlaGlyArgProProGlyGlnSerLeuGlyAlaValArgAlaAlaCysAlaGlyArg 1005
QY 1854 -----CATCCGCGCGGCCACTCAGGGCTACATGACCGCGTCAACAT 1895
Db 1006 HisLeuProValArgArgHisProArgAlaAspGlyLeuGlyLeuArgArgGlnAsp 1025
QY 1896 GTACAGCTCCTTCTACATGGCCCGCGAAGGGCGC 1931
Db 1026 ArgArgArgGlyAlaGlyProGlyArgGlyArg 1037
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RESULT 11

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US-09-252-991A-23774
; Sequence 23774, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 23774
; LENGTH: 798
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-23774
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Alignment Scores:
Pred. No.: 1.66e-14 Length: 798
Score: 309.00 Matches: 213
Percent Similarity: 30.4% Conservative: 33
Best Local Similarity: 26.3% Mismatches: 255
Query Match: 8.5% Indels: 309
DB: 2 Gaps: 47
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US-10-620-914-44 (1-1947) x US-09-252-991A-23774 (1-798)

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QY 1933 TGGCGCCCTTCGGCGGG-----CCATGTAGAGGAGC 1901
Db 16 TrpProMetAlaGlyGlySerMetAlaCysValAlaArgTrpThrProCysArg----- 33
QY 1900 TGTACATGTGACGGTTCATGTAGCCCTGAGTGGCGCGCGGAGTACGAGCGCAGTTCGA 1841
Db 34 -----ArgGlySerCys-----ArgTrpLeuAlaIleCysArgLeuArgSer 47
QY 1840 AGCCCGCCCTTCGATACGTCCGGTAGGGGGGCTG-----AGG 1800
Db 48 ValProArgSerGlyArgAlaSerArgSerThrTrpCysThrAlaProProVal 67
QY 1799 GAGCGGAGCGCCAGATGACGATGCCGCGCGCGCAACC-----TGCTTGCC 1752
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Db 68 SerThrThrArgLeuAlaThrValProProThrSerThrAlaCysAlaMetCys-TripAl 87
QY 1751 AGGCACATCGGCCAGCT-----
Db 87 aGlyCysArgProAlaAlaSerGlyProGlyAlaCysCysSerSerProAlaProGlySe 107
QY 1735 -----CGTTGGCCACGGGCATA 1719
Db 107 rThrArgArgProMetAlaAlaGlySerThrArgSerArgArgArgPheProArgSerIl 127
QY 1718 TCCA-----GCCAGTCCACGTGGTCCATCAGATCACCCTTGGTGT----- 1679
Db 127 eProAspGlySerCysSerThrProSerArgSerArgTrpThrAlaGlyTyArgLeuPr 147
QY 1678 AGGTGGCGCTTTGAGCTCCTCATGAGAGAGTGGTGGAGACGGTTCAGTTGTCAC 1620
Db 147 oAlaCysAlaTrpProAlaSerThrValArgGly-----GlySerGlyCysSerTh 164
QY 1619 ACGC-----CACTCTTGAGGGTGG-----CGAAGGCCG----- 1592
Db 164 rArgCysValArgGlyThrGlyTrpSerAlaSerArgProCysMetProThrGlySerTh 184
QY 1591 -----CCTCGCCAGGTAGTGGCGCAGTTGTGGCGCAGAACTTCCCGTGGAGGAG 1539
Db 184 rProThrMetArgProGlyCysTrpProSerCys-----CysAlaProMetPr 200
QY 1538 TTGTAGTAGAAGTAGTTCTGCTGGCGCAGTCTCGCCAGTCTCGCCACGCCCTCCATGG-- 1481
Db 200 oAlaAlaArgArgTrpArgThrAlaThrSerValSerThr-----ThrArgProTrpAr 218
QY 1480 -TGCGCGCGA-----TGATGTTCTCAATGG-----GGATGCCCTCGCCCTTGATC 1437
Db 218 gCysThrArgTrpSerThrThrCysAlaSerAlaTrpAlaSerAlaAenGlyProThrAs 238
QY 1436 AGCCGCTACTGCTTCCCGGCACGCCCGCCGCGAACCACAGACGGCTTGTGAAGAGC 1377
Db 238 nileArgTyAlaAlaProAlaAlaSerValAlaAlaThrAlaAlaProGly--ArgSe 257
QY 1376 ACCAGGCTCAGAACTTGACAAAGCCACAGCCAGCGCTGGGCCCTTCTTCCAGAG 1317
Db 257 rAlaGlyCysArg-----AlaIleProAlaThr--AlaAlaAlaThrArg-- 271
QY 1316 TGGATGAGCATGTTGCTGCCACAGACGGCGCTCTCTCCATTG-----TGGGC 1266
Db 272 -----ArgCysSerGlyThrProAspGlyCysGlnProValValGlyAlaSerLeuAl 289
QY 1265 CGTTGGCGAGCGCTTGACGGTCTTGGCCAGTCCCGACACACCGCCAGGCAGCTGCAGC 1206
Db 289 aAlaTrpArgGlyAla-----ValProCysGlyLeuLeuArgProGlyValArgPr 306
QY 1205 ACCCAGC----- 1199
Db 306 oProGlnProPheGlyLeuArgHisArgLeuAspProProArgArgArgArgLeuProva 326
QY 1198 -----ACAGCTTGGCCATGCCCGCCCTGGT-----AGTACAGCGCGCTGC 1161
Db 326 lProArgAlaAlaProCysAlaAlaGlyArgHisProValAlaAlaAspGluProGlyArgAl 346
QY 1160 TGAAGTACAGAGCGCTTGGACAGAGTGTGGCTGG-----TTTGCACAGCAG 1110
Db 346 a---ThrTyArgAlaArgArgIleArgAlaAlaGlyLeuProAspAlaLeuCysArgGl 365
QY 1109 AAGGGCGCCAGCTTCTCTCGTACAGCTCCTCAATGGCGGGTGCACGCCCTCGCCGAGAC 1050
Db 365 yAsnAlaProAlaAlaArgPro----AlaArgProGlnThrValAlaAlaArgLeuArgTh 384
QY 1049 AGCTGCCACAGCTCCTCAAACTCCAGCTGTGTAATGGCCACCTTCTTCAGCTCCAGAAC 990
Db 384 rGluProGlyArg---ArgArgGlnArgGlyGlyTrpProGlyValAlaGlyArgGlyPh 403
QY 989 GCGAGCTGCGGGGTTGACGTCCAGTCCAGCACACCTCT----- 953
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Qy	632	TCGCGCCCGAGCGCGCGCTTACTCTGGAGCAGAAAGCTGGAGCGCGTGTGGAGCGAGAACA	691
Db	164	-----SerAlaalaargAlaargGlyArgGluProSerAlaValaAlaGlyAla---Hi	180
Qy	692	CCCAGGTTTCGATCCCCTACGTGCGTGGCTCGCGCGCCCTACTACTCGTGTGGATTGGCC	751
Db	180	sProProThrAlaPro-----GlyLeuProValleuLeuLeuLeuProPr	195
Qy	752	GCCTGCCCGAGCGTTGGCCACGCGCTTCACGA-----GGAGC	787
Db	195	oProAlaargArg-----ArgAlaAlaargLeuArgThrArgArgLeuGlnProAl	213
Qy	788	CGCTGGAGCGCGCCCATGTTCCGCCCATCTTCCTGTACACGATCGTGGGAGGACC	847
Db	213	aArgPheAlaAlaAlaAlaLeuProArgThrSerProGlyGluLeuGlyAlaGlyGlnAr	233
Qy	848	CCGAGCCGGATATGGAGTGAT-----GGAGATCAACCCCAAGGACACCGTGTCTGA	898
Db	233	gArgAsnAlaAspArgGlyAspProAlaSerHisAspArgAlaargArgHisArgAlaAs	253
Qy	899	CCCTGACTAGCGCGGTGCAATGCCCTGAACCTGCTGTGCAGGGCGCGGCAGGTGG	958
Db	253	p-----ProArgProAlaGlyArgArgHisArgProArgG	265
Qy	959	TGTCGGTGGACTGCAACCCGCGAGTCGGCGCTTCTTGG-----GCTCAAGAAGGTGG	1012
Db	265	yThrArgPro--GluProAlaargGlnAlaAlaGlnGlyArgArgCysProAlaAlaAr	284
Qy	1013	CCATTCAGCAGCTGGATTGAGAGCTGTGGCAGCTGTTCGGCGAGGGCGT-----	1064
Db	284	gGlnProAlaAlaAlaargProArgArgAlaAlaGlySerArgAlaGlyArgGluProG	304
Qy	1065	-----GCACCGCGCATTCAGAGGCTGTACGAGAAGCTGGCGCCCTTCCTGT	1114
Db	304	yGlnProLeuArgProAlaHisProGly-----	313
Qy	1115	CGCAACCGAGCCCAACTTCTGGTCCAGCGCCTCTGTACTT-----	1157
Db	314	---GlyArgProAlaargLeuAlaGlnAlaGlyThrAlaValValargProGlyAlaAr	332
Qy	1158	-----CCAGCAGCGCT-----GTACTACAGGGGGCATGGCAAGCT-----	1196
Db	332	gGlyAspProAlaLeuProTrpArgLeuLeuProGlyArgArgThrGluAlaAspArgLe	352
Qy	1196	-----	1196
Db	352	uLuarArgGlyArgArgGlnProArgSerArgAlaGlyGlnArgThrValLeuAr	372
Qy	1197	-----GTGCTGGGTCTGCA-----	1211
Db	372	gProAlaAlaAspArgLeuArgArgGlyLeuAlaGlyAlaAlaLeuArgProAlaArgAr	392
Qy	1212	-----GTGCTGGCGCT-----GGTCTGGGACTGGGCAAGACCG	1246
Db	392	gAlaArgProValProGlyArgHisAlaThrGlyHisArgAlaGlyProGlyArgGlyAr	412
Qy	1247	TCAGCGCCCT-----CCCAACCGCCACATCGAGAGCAGCGCCGCTC	1291
Db	412	g--AlaProAlaTrpArgGlyValArgProAlaAlaProHisAlaGlyAlaAspProAr	431
Qy	1292	TGTGGGACGACCAATGCTCATCCATCTCGTGAAGAAGCGGCCCAAGCCGTGTGTGGC	1351
Db	431	gGlyGlnArgLeuHisargGlnPro-----ProValargThrProAlaAlaargArgSe	449
Qy	1352	TGTTCTGCAAGTTCTGAGCGCTGTGTCTTTCAA-----CAAGCCGTGC	1396
Db	449	rLeuArgGlyProArgHisGlyHisArgLeuArgArgHisArgThrAlaGlnGlyArgPr	469
Qy	1397	TGTG-----GTTCCGGCGCGGCT-----GC	1417
Db	469	oAlaPheProLeuArgArgArgArgHisArgHisProPheGlyValAlaargIleProCy	489
Qy	1418	CGGGCAAGCAGTACCGCTGATCAAGCGGACCGCATCCCCCATTTGAAACTACATCGCGC	1477

Db	489	sGlutMetArgArgAspProAlaLaGlyGlyHisArgHis-----AlaHisArgVa	507
Qy	1478	GCAC-----CATGCAGCGGTGGCGAGAACTCGCACGTGGCGCAAGCAGAACT	1525
Db	507	lHisAlaGlnProAlaLaGlyValArgThrGlyLeuArgGlyLysProAlaAspArgPr	527
Qy	1526	ACTTCTACTACAATGCCTCAC---CGGCAAGTTCCT-----CGCGCACACTGCCCA	1576
Db	527	oLeuLeuArgGluLeuArgGlnThrArgGlyValProPheHisLeuArgGlyLeuArgHi	547
Qy	1577	CTTACCTGCGGAGGCGCTTGGCCACCTCAAGAGTGGCGTGGTGGACAACTGACCG	1636
Db	547	sValProGlyProGlyLeuArgArgProLeuGlu---ProGlyGlyArgAlaAspGI	566
Qy	1637	TCTCCACCACTTCTTCATGAGAGCTCAAGCGCG-----	1673
Db	566	nGlnAlaLeuAspLeuLeuGlyValGlnAlaValAlaAArgProGlyAspLeuGlyLe	586
Qy	1674	-----CACCTACAC-----CAAGTGAATCTGA	1696
Db	586	uArgProAlaGlyProAlaLeuHisProValProSerValGlnLeuAspGlyProAlaPr	606
Qy	1697	TGGACCACTGGA-----CTGGCTGGA-----TATGC	1723
Db	606	oGlyProProGlyPheGlyAlaAspArgGlnLeuAlaGlyAspHisProAlaHisProAl	626
Qy	1724	CCGTGGCCAAAGAGCTGGCGAGTGGCTGCCAAGCAGGTTGGCGC-----	1769
Db	626	aProGlyArgArgHisAlaAspProProGlyArgArgArgAlaGluAlaLeuLeuHi	646
Qy	1770	----GGCGGCATCGTCATCTGGCGTCCGCCTC-----CCTCAGCCCGCCCT	1813
Db	646	sArgArgArgArgHisArgGlyProArgAlaAspHisArgGlnProArgArgProLe	666
Qy	1814	ACGCCGAGCTGATCCCAAGCGGGCTT-----CGACGTGCGCTGCATCCGCGCGCCA	1867
Db	666	uArgArgAlaAspArgGlnHisArgGlnProGlyGlnArgGlyGluHisProProAlaAr	686
Qy	1868	CTCAGGCGTACATGACCGCGTCAACATGTACAGCTCTTCTCATGCGCCCGCGGAAGG	1927
Db	686	gArgGlyThrAlaAlaPro-----ValArgGlyProProAlaAl	699
Qy	1928	GCGC 1931	
Db	699	aArg 700	
RESULT 13			
US-09-252-991A-20408			
; Sequence 20408, Application US/09252991A			
; Patent No. 6551795			
; GENERAL INFORMATION:			
; APPLICANT: Marc J. Rubenfield et al.			
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS			
; FILE REFERENCE: 107196.136			
; CURRENT APPLICATION NUMBER: US/09/252,991A			
; PRIOR FILING DATE: 1999-02-18			
; PRIOR FILING DATE: 1998-02-18			
; PRIOR APPLICATION NUMBER: US 60/094,190			
; PRIOR FILING DATE: 1998-07-27			
; NUMBER OF SEQ ID NOS: 33142			
; SEQ ID NO 20408			
; LENGTH: 957			
; TYPE: PRT			
; ORGANISM: Pseudomonas aeruginosa			
US-09-252-991A-20408			
Alignment Scores:			
Pred. No.: 2,31e-14 Length: 957			
Score: 307.50 Matches: 224			
Percent Similarity: 34.6% Conservative: 32			

Query Match:	30.3%	Mismatches:	280
DB:	8.5%	Indels:	204
	2	Gaps:	40
US-10-620-914-44 (1-1947) x US-09-252-991A-20408 (1-957)			
Qy	29	CGAGCTACACCAAGAAAGAACTTCTCCCTGGAGAGCTCAAGCTCAGCAGCATGAAGGATG	88
Db	128	ArgArgProAlaAaArgGThrArgPro	136
Qy	89	ACCTGACCGTTCTGCGCCATATGTGTTGCGCAGCAAGAGGCGGATGATCAGCGTGCTC	148
		:::	
Db	137	-----LeuProGlyProAlaAaSerProAla-----ThrGly	147
Qy	149	GCCTGGAGAGCTTCTACGGGCCCC-----AGCCGCTGCTTGTGCTGCCCGCC	196
Db	148	AlaGlyArgLeuProProGlyArgGlyAlaArgProLeuProAlaIleProPro	167
Qy	197	TGGCCGAGCGTCTGA-----ACCTCATCTGGTTGACC	229
Db	168	GlnSerProAlaAaArgGlyProGlyAlaAaGlyHisGlnProAlaAaAaGlyLeu---	186
Qy	230	TGGGTGGTGGCACTGGGAGAAATGTCATATGCTGGCTGATTCACGCTGGCGCAAGT	289
Db	187	-----AlaProGlyAlaProAlaProValAlaAaIleAlaAaArgThrGlnArgThr	203
Qy	290	TCAAGTCCATCTACGTGGTTCGACCTGTGCCACTCGCTGTGCGAGGTGGCCAAAGAAGAAGG	349
Db	204	GlyProAlaProAspArgArgGlyGluArgGlyAlaAspGlyArgGlnArgProArgThr	223
Qy	350	CGAAGGCCAAGGGCTGGAAGATGTCAGGTCTGGAGGCCGACGCTGCCAATTGCGC	409
Db	224	ArgArgGlyArgAlaGlyArgAlaAaArgAlaGlnArgArgLeuGlyArgArgAlaAa	243
Qy	410	CCCCTGAGGACCGCGACGCTCATCCTTCTCTACTCGCTCAGCATGATTCACCGT	469
Db	244	ProLeuAlaAlaGlyAlaArgArgSerArgGlyAlaGlyGlnProArg-----	259
Qy	470	TCCACAACGTCAATCACACAGGCTTCTCGTACTCTGCCAAGACGCGCTGGTGGG---	524
Db	260	-----GlyThrArgArgArgArgThr-AspProArgLeuProAlaGlyGlyGly	275
Qy	525	----CGTTGCCACTTCTACGTAGCGGCAAGTACGACCTGCCCTCGCGCCAGAT---	577
Db	275	YAspArgAlaAlaAlaAaArgGlyProGlyVal-----ProArgProAspArgAl	292
Qy	578	CCTGGTCGCGCGGTTCTTCTGGCCATCGATCTTCGACATCGACAACATTGATCGCGC	637
Db	292	aLeuArgAla-----LeuLeuArgArgAlaAaArgGlyArgGlyArgArgGly	310
Qy	638	CCGA-----GCGCGCGCTCTACCTGGAGCAGAGCTGGAGC	673
Db	310	naRGlyAspProArgProProAlaAaAlaProGlyLeuProArgAlaAaGlyArgGly	330
Qy	674	CGGT-----GTGGGAGCAGAACACACC	694
Db	330	sArgProValValProLeuProProValLeuArgProAlaAlaGlyAlaSerLeuAl	350
Qy	695	AGGTTTCATCCCTACGTGCGGTGTCGCGCCCCCTCTACTAGTGTGGATTGCGCGCC	754
Db	350	aArgLeuArgSerValArgLeuProAlaProAlaArgLeuArgLeuValGlnProPr	370
Qy	755	TGCCAGCGTTGGCCACCGCCCTGCACGAGGAGCGCTGGAGCGCGCCCGCCAT---	806
Db	370	o-----TrpProAlaArgProGlyGlyGlyAlaGlyAlaAaArgArgProAlaGly	387
Qy	807	-----GTTCCCGCCACCTTCTCTGTA---CACCGAGTCGTGGGAGGA-----	845
Db	387	YArgGlyGlyGluProGlyAlaGluProValGlyArgAlaThrAlaGlyGlyAlaGluHi	407
Qy	846	-----CCCCAGCCGGATATGGAGTGTAGAGATCAACCCCAAGACACGGTGTCTGA	898
Db	407	sArgHisProAlaAlaLeuGluAspGlyProAlaGlyGlnProPropGlyGluHiAlaAl	427

QY	899	CCCTGA	CTAGCGCGGTGCAATGCCCTGA	CCTGCTT-----GGTGCAGGG-----GG	946
Db	427	aProAsp	-----ProAlaVal	ArgLeuGlyAlaGlyAlaG	439
QY	947	CCGCCCA	GGTGTCTCGGTGGAGCTGCAACCCCGCAGTGGCGCTTCTCGAGCTGAAGA	1006	
Db	439	YLeuProAlaGlyCysArgGlyArgThrGlyArgProThrGlyAlaPheProAlaGlyAl	459		
QY	1007	AGGTGGCC	CAATTCAGCAGCTGAGTTTGAGACGCTGTGGCAGCT-----	1049	
Db	459	aGlyArgValArgAlaAlaArgProAlaGlyProValAlaGlyProGluArgGlyAsp	479		
QY	1050	-----GTTCCGGC	GAGCGCTGCACCCCGCATTTGAGGAGCTGTACGAGA	1093	
Db	479	gAlaArgProArgArgTyrArgGlnGlyArgGlyAlaLeuProArgGlyLeuAlaGlyPr	499		
QY	1094	AGAAGCTGGCGCCCTT-----CCTGTC-----GCAACACAGCA-----	1127		
Db	499	oArgArgGlyAlaLeuThrPHisProProAlaMetProValAspAlaGlnProGlyG	519		
QY	1128	-----CAACTCT	TGTTCCAAAGCGCTCTGTGTTACTTCCAGCAGCGCT---GPACT	1174	
Db	519	yAspProTyrArgLeuLeuAlaGlyAlaGlnLeu---GlnProArgArgProGlyVal	538		
QY	1175	ACCAGGCGGCATGGCAAGCTGTGCTGGGTGCTGCAGTCCCTGGCGTGGTCTCGGAC	1234		
Db	538	gProAlaLeuArgGlnProAlaVal-----ArgGlyThrGlyPr	551		
QY	1235	TGGCAGACGGTCAAGCGCT-----CGCCAAGCGCCACAACTGGAGAGC	1282		
Db	551	oLeuArgProArgProArgProGlyAlaArgArgGlyGlyAlaArgArgGlyGlyG	571		
QY	1283	AGCGCGCTGCTGGGA-----CAGCAACATGCTCATCTTCGTGAAGAAGC	1330		
Db	571	yAlaProGlyProGlyThrProProAlaProAlaGlyAlaThrProLeuArg-----G	589		
QY	1331	GGCCCAAGCGCTGTGTGCTGTCTGAAGTTCTGAGCTCTGTGCTCTTCAACAAGG	1390		
Db	589	yAlaArgAlaAlaProAlaValProArgLeuProAlaGlnProGlyAla-----	605		
QY	1391	CCGTGCTGTGGTTCGGCGGGCGTCCGGCAGCAGTACGGCTGTATCAAGCGCGAGC	1450		
Db	606	-----AlaAlaGlyArgSerAlaGlnValAspGlnAlaGlyAs	618		
QY	1451	GCATCCCATTTGAACTACATCGCGGCACCATGA-----CGCGCTGGCGGAGA	1501		
Db	618	nArgGlyAsnProGlnLeuProGlyCysGlnProGlyAspArgLeuLeuArgProGlyG	638		
QY	1502	ACTCGCAGTGGCGCAAGCAAGTACTTCTACTACAACTGCCT-----CACCGGCA	1552		
Db	638	nProGlyArgAlaProGlyGlnLeuArgGlyValArgProAlaTrpArgArgAl	658		
QY	1553	AGTT-----CCTGCGCAACCTGCCCCCACTACCTGCGCGAGCGCG	1594		
Db	658	aValAspAlaCysLeuGlyTyrProAlaAspLeuLeuPro-----G	672		
QY	1595	CCTTCGCCACCTCAAGAGTGGGT-----GGTGGACAACCTGACCGTCTCCACCA	1645		
Db	672	yGlyAspHisProAspGlnValArgThrLeuAlaGlyProGlyProAspArgThrGly	692		
QY	1646	ACTTCTTCATGGAGGAGCTCAAAGCGCGCACCTACACCAAGGTGATTCTGATGGACCA	1705		
Db	692	gArgLeu---AlaThrAlaProGlyArgHisLeu-----Ar	703		
QY	1706	TGGACTGGCTGGATATGATCCCGTGCACCAACAGTGGCCGAGTGCCTGGCCACAGCTTG	1765		
Db	703	gTrpAlaGlyGlyHisAlaAlaGlyMetGlnSer-AlaAlaAlaAlaCysGlyVal	723		
QY	1766	CGCGCGCGGCGATGTCATCTGGCGTCCG-----CCTCCCTCAGCCGCCCTACG	1816		
Db	723	laProGlyArg-----ProGlyAlaProArgArgThrProGlyGlySerArgProAla	740		

Qy 1817 CCGAGCTGATCCAGAGCGGGCTTCGACGTGCGCTCATCCGCGCGCCACTCAGGCT 1876
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Db 741 Pro-----GlyProAlaGlyProLeuAspAla 749
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Qy 1877 ACATGGACCGGTCAACATGTACAGTCTCTTACATGGCCCGCGGAGGCG 1930
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Db 750 GlyGluArgArgValAlaAlaGlySerProGlyProArgProThrGlyArgAla 767
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RESULT 14
US-09-252-991A-18035
; Sequence 18035, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 18035
; LENGTH: 783
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-18035

Alignment Scores:
Pred. No.: 4,58e-14 Length: 783
Score: 303.00 Matches: 225
Percent Similarity: 35.2% Conservative: 45
Best Local Similarity: 29.4% Mismatches: 277
Query Match: 8.4% Indels: 220
DB: 2 Gaps: 45

US-10-620-914-44 (1-1947) x US-09-252-991A-18035 (1-783)

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Db 2 SerLeuProThrAlaArgPro-----ArgSerArgGlyAlaAspArg 15
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Qy 1885 GGTCTAGTACCTCTAGTGTGCGGGCGGATGCACGCAGCTCGAAGCCGCTTCTGGA 1826
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Db 16 GlnProThrGluPro-----AlaArg-----ProProAlaAla 26
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Qy 1825 TCAGCTCGGCTAGGGCGGGCTGAGGAGG---CGGAGCGCAGATGACGA----- 1778
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Db 27 GlyArgArgValProAlaGlyLeuGlyArgGlyArgAlaValGlnProArgProAlaGly 46
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Qy 1777 TGCAGCGCGG-----GGCAACCT-----GCTTGG 1754
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Db 47 LeuArgProCysLeuLeuHisProGlnGlyGlnArgAlaAspProLeuArgAlaVal 66
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Qy 1753 CCAGGCACTCGGCGAGCTCTGTGGCA---CGGGCATATCAGCGAGTCCACGCTGTCCA 1697
|||
Db 67 ProAlaGluArgProAlaArgThrProGlyLeuAlaArgAlaGlyGlyGlyAla 86
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Qy 1696 TCAGAACTCACCTTGTGTAGTGTGCGGCTTTGAGCTCTCCATGAAGAAGTTGTGGAGA 1637
|||
Db 87 ArgGluAspLeuAlaValArgGlyThrArgArgLeuProValAspArgArg---TyrArg 105
|||
Qy 1636 CGGTCAAGTTGTCCACACCGCACTTTTGGAGGTGG----- 1601
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Db 106 ArgAlaGlyArgArgArgProAlaProGlyLeuArgGlyIleGluGlyLysThrArg 125
|||
Qy 1600 ---CGAAGCGCGCTCGCGCAGGTAGGTGGGCGAGTGTCTCGCGCAGGAACCTGCGGTGA 1544
|||
Db 126 ArgArgArgProValArg----- 131
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Qy 1543 GGCAGTTGTAGTAAGTAGTTCTGCTTGCAGCATGTGCGAGTTCTCCGCCACGCGGTCCA 1484
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Db 132 -----GlnArgThrGlnAlaSerAlaAlaArgProSerAlaProHisArg----- 146
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Qy 1483 TGGTGGCGCGATAGTTCTCAATGGGATCGCTCGCGCTTGTATCAGCGCGTACTGCT 1424
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Db 147 -----TyrArgGlnPheAlaGlnArgGlyGlyAspProArgHisHisGlnArgValSer 164
|||
Qy 1423 TGCCCGCAGCGCGCGCCGCAACACACAGCAGCGGCT---TGTTGAAGAGCACCGAGGTCA 1367
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Db 165 ProProSerThrAlaGlyArg-----AlaAspProGlyAlaHisArgSerProGlyPro 182
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Qy 1366 CGAACTTTGACGACAGCAGCACACAGCGCTTGGCCGCTTCTTCCAGAAAGTGGATGACGA 1307
|||
Db 183 ArgGlyArgArgThrAspArgProAlaAla---AlaThrGlyArgProAlaGly----- 199
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Qy 1306 TGTGTGCTCCACAGAGCGGCGCTCTCTCATTTGGGCGCTTGGCGAGGCGCTTG- 1248
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Db 200 -----LeuArgAlaAspProGlyProTrpArgArgPheProGlyArgPro 215
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Qy 1247 ACGGTCTTGGCCAGTCCACAGCACCGCGCC-----AGCAGCTGCAGCACCC 1203
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Qy 1202 CAGCACAGCTTGGCCATGCCCGCTGTGTAGTACAGGCGCTGTGGAAGTACAGAGGCGC 1143
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Qy 1142 TTGCACCAAGTTGTGGCTGTTTGCACAGGAGGGCGCCAGCTTCTTCTCGTACAGC 1083
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Qy 1082 TCCTCAATGCGCGGTGCACGCCCTCGCGCA---ACAGTCCACACAGCTCTCAAACTCC 1026
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Qy 1025 AGTCTGAAATGGCCACTTCTTTCAGTCTCAGAGCGCGCTGCG----- 980
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Db 297 aProGlyArgArgArgProProAlaProSerArgArgThrProAlaProAlaGlyAl 317
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Db 317 aAlaProGlyArgProGlyHis-----AlaProAlaProCysLeuArg 331
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Db 331 gAlaProAlaGlyGlyProProArgThrPro-----GlyProProGlyAspAl 347
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Qy 782 TCGT-----CGAGGCGTGGCCAACTGGCGAGCGCGCAATCCACAGCTAGTAG 732
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Db 367 oArgArgAlaProAlaAlaArgArgProArgGlyThrGluGlySerSerSerAlaProAr 387
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Qy 731 GGGCGCGCAGCCACGCGACGTAGGGATCGAACCTGGGTGTCTGCTCCACACGCGC 672
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Db 387 gArgThrGlyAlaAspAlaGlnArgGlyGlnProAlaGlyAspProGlyProArg----- 405
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Qy 671 TCCAGCTTCTCTCAGTAGCGCGCGCTCGGGCGGATGTCAATGTTGCGATGTCG 612
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Db 406 ----LeuGlnHisProProArgArgAlaTrpProGlyAsp-----ProArgCysAr 421
|||
Qy 611 AAGATCATCGCC-----AGAAGAAACCGCGC 585
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Db 421 gProAspProAlaGlyThrAlaProGluGlyAlaProArgGlyArgArgThrGlyGlyAl 441
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Qy 584 GACCAGGCGCATCTGGCGCAGGGGAGGTCTGCTACTTGGCGCTCACGTAGTAGTCGCAACG 525
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Db 441 aGlyArgGlyGlnProProAspAlaGlyAspProValAlaAlaGlyLeuSerArgAspAs 461
QY 524 CCACACAGCGCTTTGGACAGAGTACGAGCAAGCCTGCTCGATGACCTGTGGAAACGGT 465
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QY 464 GGAATCATCGTCAGCAGTACGAGAGAGGTGATGACGCTCGCGGTCCCTCAGGGGGCCCA 405
Db 476 oProArgPheSerAlaProArgArg-----ProAlaProGluHisArgPr 491
QY 404 AATTGGCAAGCGCTGGCCTCCACAGA---CCTGGACATTCTCCAGCCCTTGCGCTTCGCC 348
Db 491 oLeuGlyHisGlnProAlaAlaArgGlnProGlyGlyThrSerArgArgAlaPro---Pr 510
QY 347 TTCCTCTTGGCCACT-----CCACAGCGAGTGGC----- 317
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QY 316 -----ACAGTGCACACAGCTAGATGGACTTGAACCTTGCAGGCTCATGTAATCA 267
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QY 266 GCCATCATATGCACATTCTCC-----CAGTGGCCAC----- 236
Db 550 aAlaProGlyGlnGlyAlaProGlyGlyArgArgGlyLeuHisArgArgProAspLeuPr 570
QY 235 -----CACCCAGGTCAACCCAGA-----TG 216
Db 570 oAlaIleAlaGluLeuHisProAlaLeuProAlaHisArgAlaGlyGlyProHisGlyAr 590
QY 215 AGGTTGAGCGCTCGGCAGCGGGGCGAG---CAAAGGAGCGGCGCTGGG----- 170
Db 590 gGlyGlnArgArgArgGlyAlaGlyGlnGlyArgArgArgProGlyProGlyLeuAr 610
QY 169 -----GCCGTAGAAAGCTCTCCAGCGAGCGAGCGTGA 138
Db 610 gProGlyArgGlyArgArgThrGlyArgAlaArgArgHisProAlaProArgProAs 630
QY 137 TCAT---CGCCCTTCTTCTGCTCCGAAACACATATATGGCGCAGAACGGTCAGGTCTCTTC 81
Db 630 pHisProArgGlnProCysProArgArgThr-----ProArgArgGly----- 644
QY 80 ATGCTGTGACTTGAGCTTCTCCAGGAGAGAGTCTTCTTGGTGTAGCTCGCAGGCGGG 21
Db 645 -----AlaAspAlaArgAlaAlaGlnArgValAlaGlyValAspProGlnGlnHi 661
QY 20 CCGTCACGACCGCGCC 5
Db 661 sArgHisGlyProThr 666

RESULT 15

US-09-252-991A-26099
; Sequence 26099, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 26099
; LENGTH: 863
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-26099

Alignment Scores:

Pred. No.: 5.65e-14 Length: 863
Score: 302.00 Matches: 227
Percent Similarity: 29.8% Conservative: 29
Best Local Similarity: 26.5% Mismatches: 252
Query Match: 8.3% Indels: 350
DB: 2 Gaps: 50
US-10-620-914-44 (1-1947) x US-09-252-991A-26099 (1-863)
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Db 86 SerHis-----ProProAspGlyGlnGlnAlaProValGluAspArgHisAlaArgArg 103
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Db 124 ArgGlyArgThrHisArgLeuProThrAspAspGlnGlnArgArgArgArgPro 143
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Db 184 Ala-----ProCysGlyAspProGlyValArg-----ArgProPro 195
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Db 196 -----ArgGlnProAlaLeuProArgArgThrArgLeuLeuGlyAlaAla 210
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Db 211 ProProGluGlyHisArgGlySerSerLeuProGly----- 223
QY 1534 AGTAGAAGTAGTTCTGCTTCCGCAACGTGCTCCGCGCACCGCTTCCGCGCACCGCTTCCATGTCGCGC 1475
Db 224 -----AlaArgCysArgProAlaSerArgHisGlyArgGlyGlyGlyGly 239
QY 1474 CGATGTAGTTCTCAATGGGATGCCCTCCGCTTGATCAGCGCGTACTGCTTGGCCCGCA 1415
Db 240 ArgGlyPheGlyGlnLeuArgGlyArg----- 248
QY 1414 CGCGCGCGCGAACCACAGCACAGC----- 1391
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 Qy 691 TGTCTGCTCCACAGCGCTCCAGCT----- 665
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Search completed: May 5, 2006, 07:53:02
 Job time : 78 secs

GenCore version 5.1.7
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OM nucleic - protein search, using frame_plus_n2p model

Run on: May 5, 2006, 07:51:18 ; Search time 28.5 Seconds
(without alignments)
5708.868 Million cell updates/sec

Title: US-10-620-914-44

Perfect score: 3619

Sequence: 1 atggggcggtcgctgacgg.....gcgccaagaagacaactaa 1947

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
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Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 3735138

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Published Applications AA Main:

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6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	891	24.6	752	5	US-10-741-849-7021
3	850.5	23.5	908	4	US-10-620-914-50
C 4	476.5	13.2	19662	4	US-10-084-846A-6
5	459	12.7	19723	4	US-10-084-846A-5
C 6	457.5	12.6	19652	4	US-10-084-846A-7
C 7	456.5	12.6	19608	4	US-10-084-846A-8
8	446	12.3	19608	4	US-10-084-846A-3
9	443.5	12.3	19695	4	US-10-084-846A-8
C 10	436	12.0	19608	4	US-10-084-846A-3
C 11	424	11.7	19725	4	US-10-084-846A-4

12	407	11.2	19725	4	US-10-084-846A-4	Sequence 4, Appli
C 13	383.5	10.6	19695	4	US-10-084-846A-3	Sequence 3, Appli
14	379.5	10.5	416	4	US-10-118-495-3	Sequence 3, Appli
15	379.5	10.5	416	4	US-10-620-914-3	Sequence 3, Appli
C 16	370	10.2	900	5	US-10-450-763-33892	Sequence 336, App
17	366.5	10.1	1084	5	US-10-794-514A-336	Sequence 336, App
C 18	357	9.9	1084	5	US-10-794-514A-336	Sequence 336, App
C 19	352	9.7	599	5	US-10-450-763-33889	Sequence 33889, A
20	342.5	9.5	19662	4	US-10-084-846A-6	Sequence 6, Appli
21	341.5	9.4	437	4	US-10-437-963-132079	Sequence 132079,
22	335.5	9.3	465	4	US-10-437-963-174113	Sequence 174113,
23	326.5	9.0	416	4	US-10-118-495-29	Sequence 29, Appl
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25	321	8.9	415	4	US-10-118-495-41	Sequence 41, Appl
26	321	8.9	415	4	US-10-620-914-41	Sequence 41, Appl
27	320.5	8.9	19652	4	US-10-084-846A-7	Sequence 7, Appli
28	308	8.5	455	4	US-10-437-963-161457	Sequence 161457,
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43	303.5	8.4	4440	4	US-10-176-482-525	Sequence 525, App
44	303.5	8.4	4440	4	US-10-176-757-525	Sequence 525, App
45	303.5	8.4	4440	4	US-10-176-913-525	Sequence 525, App

ALIGNMENTS

RESULT 1

US-10-620-914-45
; Sequence 45, Application US/10620914
; Publication No. US20040093639A1
; GENERAL INFORMATION:
; APPLICANT: Benning, Christoph
; APPLICANT: Riekhof, Wayne
; APPLICANT: Klug, Rouven
; TITLE OF INVENTION: Compositions and Methods for the Production of Betaine Lipids
; FILE REFERENCE: MSU-07769
; CURRENT APPLICATION NUMBER: US/10/620,914
; CURRENT FILING DATE: 2003-07-16
; PRIOR APPLICATION NUMBER: 10/118,495
; PRIOR FILING DATE: 2002-04-08
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 45
; LENGTH: 648
; TYPE: PRT
; ORGANISM: Chlamydomonas reinhardtii
US-10-620-914-45

Alignment Scores:
Pred. No.: 1.73e-204 Length: 648
Score: 3463.00 Matches: 648
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 95.7% Indels: 0
DB: 4 Gaps: 0

US-10-620-914-44 (1-1947) x US-10-620-914-45 (1-648)

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QY 1321 GTGAGAAACGGGCCCAAGCGCTGGTGTCTGCTCAAGTTCGTGAGCTCGTGTCTC 1380
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Db 641 ArgLysGlyAlaLysLysAspAsn 648
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; Sequence 7021, Application US/10741849
; Publication No. US20050019931A1
; GENERAL INFORMATION:
; APPLICANT: Roemer, Terry
; APPLICANT: Jiang, Bo
; APPLICANT: Boone, Charles
; APPLICANT: Bussey, Howard
; TITLE OF INVENTION: Nucleic Acids Encoding Anti-fungal Drug Targets and Methods of
; TITLE OF INVENTION: Use
; FILE REFERENCE: 10182-023-999
; CURRENT APPLICATION NUMBER: US/10/741,849
; CURRENT FILING DATE: 2003-12-19
; PRIOR APPLICATION NUMBER: US 60/434,832
; PRIOR FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 8000

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 7021

; LENGTH: 752

; TYPE: PRT

; ORGANISM: Candida albicans

US-10-741-849-7021

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Db 110 IleTrpIleAspIleGlyGlyThrGlySerAsnIleGluPheMetAspGluIleSer 129
QY 277 GACCTGGCGAG---TTCAAGTCCATCTACGTCGTGCGACCTGCCACTCGCTGCGGAG 333
Db 130 LysIleSerGluAsnPheLysAlaValTyrLeuValAspLeuSerProSerLeuCysGlu 149
QY 334 GTGGCCCAAGAAAGAGCGCAAGCGCTGGAGAAATGTCAGGTCTGGAGCGCGAC 393
Db 150 ValAlaLysAlaArgPheGluAlaHisIleTrpThrAsnValHisValLeuValAlaAsp 169
QY 394 GCTTGCCTCAATTTGGCCCTTGAGGGACCGCGACGCTCATCATCTCTCTCTCTCTCT 453
Db 170 AlaCysAspPheThrIleAspTyrAspSerAlaAspLeuIleThrPheSerTyrSerLeu 189
QY 454 ACGATGATTCACCGCTTCCCAACGTCATCGACACGAGCTTCTGCTACCTGTCCTCCAGAC 513
Db 190 SerMetIleProThrPheAsnAlaAlaIleAspAsnAlaValSerLysLeuAspMetGlu 209
QY 514 GGCCTGGTGGCGGTGGCGACTTCTACGTGAGC-----GGCAAGTAC 555
Db 210 GlyIleIleAlaThrValAspPheGlyIleGlnSerSerAspThrSerMetGlyArgIle 229
QY 556 GAC-----CTGCCCTCGCCAGATGCGCTGGTGGCGCGCTTCTCTGCGGA 603
Db 230 AsnThrValGlyLeuValAsnArgAspIleProTrpIleLeuArgAsnPheTrpArg 249
QY 604 TCGATCTTCGACATCGACACATTCATCGGCCCGCGCGCGCTACCTCGGAGCAG 663
Db 250 IleTrpPheGluAlaAspLysValPheLeuAspSerSerArgAsnTyrLeuGluTyr 269
QY 664 AAGCTGGAGCGCGTGGGAGCAGAACACCCAG-----GGTTCGATCCCTAC 711
Db 270 LysPheGlyThrValLysSerLeuAsnSerTyrAsnLysAlaLeuGlyLysIle----- 287
QY 712 GTGCCGTGGTGGCGCCCTACTAGTGTGGATTTGGCCGCTGCGCCAGCTTGGCCAC 771
Db 288 -----ProTyrTyrIleTrpIleGlyCysAspLysSerLysSerHis 301
QY 772 GCCCTGCACGAGGAG-----CGCTGGAGCGCGGCCCATGTTCCCGCCACC 819
Db 302 ThrIleLeuGluArgLeuAsnCysLeuAlaThrGluSerProTyrLeuAlaProThrThr 321
QY 819 ----- 819
Db 322 ThrProIleAlaAsnGlnLeuGluAspIleProIleSerLysGlyHisGluAlaAlaLeu 341

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QY 819 ----- 819
Db 342 IleAsnLeuGlnLysAsnLeuProTyrProSerMetTyrTyrGlnLysGluTyrTrpArg 361
QY 820 -----TTCTCTGTACACG 831
Db 362 ValTyrTyrAspGluMetAsnProLeuTyrGluGlnPheLysAsnGlnTyrIleTyrAla 381
QY 832 CAGTCGTGGGAGACCCCGAGCCGATATGGAGGTGATGGAGATCAACCCCAAGACACG 891
Db 382 PheThrTrpGluAspProArgGluAspHisLysLeuLeuAsnPheThrSerAspAspThr 401
QY 892 GTGCTGACCTGATAGCGGGCTGCAATGCTCCCTGAACCTG-----CTGGTCAGGGG 945
Db 402 ValLeuAlaIleThrSerAlaGlyAspAsnIleLeuSerTyrAlaSerLeuProThrPro 421
QY 946 GCCGGCCAGGTGGTGGTGGACTGCAAGCCCGCAGTCGGCGCTTCCTGAGCTGAAG 1005
Db 422 ProLysLysIleHisAlaValAspLeuAsnProCysGlnAsnHisLeuLeuGluLeuLys 441
QY 1006 AAGGTGGCCATTACAGCAGCTGGAGATTGAGAGCGTGTGGCAGCTGTTTCGGCGAGGGGTG 1065
Db 442 LeuAlaSerPheArgCysLeuSerGlnGluGlnIleTrpSerMetPheGlyGluGlyLys 461
QY 1066 CACCCGCGCATTTAGGAGCTGTACGAGAAGAGCTGGCGCTCTCTCTGTCGCAACACG 1125
Db 462 IleGluAsnPheAsnAspLeuIleAspThrLeuAlaProHisMetSerSerAsnAla 481
QY 1126 CACAACCTTCGTGCTCAAGCGC-----CTCTGGTACTTCCAGCAGCGCTGTACTACG 1179
Db 482 PheGlnTyrTrpMetAspLysGlyProLysThrPheSerGlyLysGlyLeuTyr----- 499
QY 1180 GCGCGCATGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1230
Db 500 ---AspThrGlyPheSerArgTrpAlaLeuArgLeuSerArgTyrValPheLysValCys 518
QY 1231 GGACTGGGCAAGACCGTCAAGCGCTCGCCCAACGCGCCCAATGGAGGAGCAGCGCGGT 1290
Db 519 GlyValSerLysTyrValGluGluLeuCysAlaAlaThrThrMetGluGluGlnLeuArg 538
QY 1291 CTGTGGGACAGCAACATGCTCATCTTCTGTGAAGAAGCGGCCCAAGCGCTGGTGGTGG 1350
Db 539 IleTrpAsnGluHisLeu-----LysProThr----- 547
QY 1351 CTGTTCGTCAAGTTCTGTG---AGCCTGTCTCTTCAACAGCGCTGTGTGTGGTGGC 1407
Db 548 LeuPheAsnProValValGlySerLeuValGlyAsnProMetPheLeuTrpLysAla 567
QY 1408 GCGGGCTGGCGGCAAGAGTAGCGCTATCAAGCGGACGCGCATCCCATTTGAGAAC 1467
Db 568 LeuGlyValProAlaAsnGlnAlaLeuMet-----GlyProSerValIleLys 584
QY 1468 TACATCGCGCGCACCATGGAGCGGTGGCGAGAACTCGCACGTGGCGCAAGCAGAACTAC 1527
Db 585 TyrValValAspThrLeuAspProIleIleLysArgSerMetIleSerAsnAspAsnTyr 604
QY 1528 TTCTACTTACAACTCCCTCACCGCAAGTCTCTGCGGACAACTGCCCACTCTCTCTGCGC 1587
Db 605 PheTyrTyrLeuCysMetMetGlyArgTyrThrLysAsnAsnCysProAspTyrLeuThr 624
QY 1588 GAGCGCGCTTCCGCCACCTCAAG-----AGTGGCGTGGTGG 1623
Db 625 ThrLysGlyPheAsnArgLeuSerSerThrAlaAlaThrAlaSerGlySerSerProIle 644
QY 1624 GACAACCTGACCTCTCCCAACTTCTTCATCGAG-----GAGCTCAAGACCGCG 1674
Db 645 AspAsnLeuArgIleHisThrAspThrLeuAsnGluValPheGlyArgLeuLysGluLys 664
QY 1675 ACCTTACCAAGGTGATTTCTGATGGACCAAGTGGAGCTGGCTGGAT-----ATGCC 1725
Db 665 SerIleThrIleAlaIleIleMetAspHisMetAspTrpPheAspProAsnGlyArgAsp 684
QY 1726 GTGGCCCAAGAGCTGGCGGAGTGCCTGGCCCAAGAGGTGGCGCGGCGGCGATCGTCATC 1785

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Db      685 AlalLeuGluIleThr---AlalLeuLysArgCysLeuAlaProGlyGlyArgValLeu 703
      |||||::: ||| ::: |||||::: |||||::: |||||:::
Qy      1786 TGGGCTCCGGCTCCTCAGCCCGCCCTACCGCAGCTGATCCAGAGCGGGCTTC--- 1842
      |||||::: |||||::: |||||::: |||||::: |||||:::
Db      704 LeuArgSerAlaSerThrLysProTrpTrpLysThrPheLysAsnLeuGlyPheGln 723
      |||||::: |||||::: |||||::: |||||::: |||||:::
Qy      1843 GACGTGGCGCTCANTCCGCGCGCCACTCAGGCTACATGGACCGCTCAACATGTACAGC 1902
      ::::: ||| ::::: |||||::: |||||::: |||||:::
Db      724 GluGluGluAsnValAlaArgGlnProGlySerSerIleAspArgValAsnMetCysAla 743
      ::::: ||| ::::: |||||::: |||||::: |||||:::
Qy      1903 TCC 1905
      :::
Db      744 Asn 744

RESULT 3
US-10-620-914-50
; Sequence 50, Application US/10620914
; Publication No. US20040093639A1
; GENERAL INFORMATION:
; APPLICANT: Benning, Christoph
; APPLICANT: Riekhof, Wayne
; APPLICANT: Klug, Rouven
; TITLE OF INVENTION: Compositions and Methods for the Production of Betaine Lipids
; FILE OF INVENTION: MSU-07769
; CURRENT APPLICATION NUMBER: US/10/620,914
; CURRENT FILING DATE: 2003-07-16
; PRIOR APPLICATION NUMBER: 10/118,495
; PRIOR FILING DATE: 2002-04-08
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 50
; LENGTH: 908
; TYPE: PRT
; ORGANISM: Neurospora crassa
US-10-620-914-50

Alignment Scores:
Pred. No.:      8,65e-44      Length:      908
Score:          850.50      Matches:      222
Percent Similarity: 44.7%      Conservative: 105
Best Local Similarity: 30.4%      Mismatches: 235
Query Match:      23.5%      Indels:      169
DB:              4          Gaps:      18

US-10-620-914-44 (1-1947) x US-10-620-914-50 (1-908)
Qy      205 CGCTCGAACCTCATCTGGGTTGACCTGGGTGGTGGCACTGGGGAGAATGTCGATATGATG 264
      |||||::: |||||::: |||||::: |||||::: |||||:::
Db      178 ArgArgLysProIleTrpValAspValGlyGlyGlyThrGlyTrpAsnIleGluAlaMet 197
      |||||::: |||||::: |||||::: |||||::: |||||:::
Qy      265 GCTGATTACATCGACTGGCGAAG---TTCAAGTCCATCTACGTGTGTCGACCTGTGCCAC 321
      |||||::: |||||::: |||||::: |||||::: |||||:::
Db      198 AlalLysPheValAsnValSerGluPhePheLysThrValTyLeuValAspPheSerPro 217
      |||||::: |||||::: |||||::: |||||::: |||||:::
Qy      322 TCGCTGTGCGAGGTGGCCAAAGAGAGCGAAGGCCAGGCTGGAAGAATGTCAGATC 381
      |||||::: |||||::: |||||::: |||||::: |||||:::
Db      218 SerLeuCysGluValAlaAlaArgLysArgPheAlaArgLeuGlyTrpGluAsnValArgVal 237
      |||||::: |||||::: |||||::: |||||::: |||||:::
Qy      382 GTGGAGGCGCGAGCTTGGCAATTTGCG-----CCCCCTGAGGGGACCC 423
      ::: |||||::: |||||::: |||||::: |||||:::
Db      238 IleCysThrAspAlaAlaArgLysPheArgLeuGluAspTyLeuValAspValAspGlyGlu 257
      ::: |||||::: |||||::: |||||::: |||||:::
Qy      423 ----- 423
Db      258 SerGlySerGlyAspSerSerProSerLeuSerGlyTrpTrpGlyGluThrLysProGly 277
      |||||::: |||||::: |||||::: |||||::: |||||:::
Qy      424 -----GGAGCGCTCATACCTTCTCTACTCGCTCAGCATGATTCACCGGTC 471
      |||||::: |||||::: |||||::: |||||::: |||||:::
Db      278 ArgHisAlaGlyAlaGluLeuIleThrMetSerTySerLeuSerMetMetProAspTy 297
      |||||::: |||||::: |||||::: |||||::: |||||:::
Qy      472 CACAACTCATCGACCGGCTTGTCTGTCGTACTGTCTCCCAAGACGCGCTGGTGGCGGTGCC 531
      ::::: |||||::: |||||::: |||||::: |||||:::

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Db      298 PheSerIleIleAspSerLeuGluSerLeuAlaProHisGlyLeuIleAlaValVal 317
      |||||::: |||||::: |||||::: |||||::: |||||:::
Qy      532 GACTTCTACGTGAGCGGCAAGTACGAC-----CTGCCC 564
      |||||::: |||||::: |||||::: |||||::: |||||:::
Db      318 AspPheTyAlaGlnSerLysValAspPheThrPheArgAsnTyThrGlyGlyLeuMet 337
      |||||::: |||||::: |||||::: |||||::: |||||:::
Qy      565 CTGCGCCAGATGCTCGTGGCGCGCTTCTCTGGCGATCGATCTTTCGACATCGACAAC 624
      |||||::: |||||::: |||||::: |||||::: |||||:::
Db      338 AsnArgHisValGlyTyPheAlaAlaArgAsnPheTrpArgSerTrpPheAspAlaAspArg 357
      |||||::: |||||::: |||||::: |||||::: |||||:::
Qy      625 ATTGACATCGGCGCCGAGCGCGCTCTACTGTGAGCAGAAAGCTGGAGCGCGGTGG--- 681
      ::: |||||::: |||||::: |||||::: |||||::: |||||:::
Db      358 ValSerLeuGluProAlaAlaArgAspTyLeuGluTyArgPheGlyThrValLeuThr 377
      |||||::: |||||::: |||||::: |||||::: |||||:::
Qy      682 -----GAGCAGAACACCCAGGGTTCCATCCCTACGTCGCGTGG-----CTG 723
      |||||::: |||||::: |||||::: |||||::: |||||:::
Db      378 ValAsnAlaArgAsnAsnThrLeuGlyAlaIleProTyTyTrpLeuGlyCysLeu 397
      |||||::: |||||::: |||||::: |||||::: |||||:::
Qy      724 CGCGCCCTTACTACGTG----- 741
      |||||::: |||||::: |||||::: |||||::: |||||:::
Db      398 LysLysProPheSerThrSerSerLeuProHisGluIleValGluHisIleAspAlaIle 417
      |||||::: |||||::: |||||::: |||||::: |||||:::
Qy      741 ----- 741
      |||||::: |||||::: |||||::: |||||::: |||||:::
Db      418 AlaThrGluSerProArgSerSerProArgLeuValGlyLysHisSerSerSerAlaThr 437
      |||||::: |||||::: |||||::: |||||::: |||||:::
Qy      742 -----TGGATTGGCCGC----- 753
      |||||::: |||||::: |||||::: |||||::: |||||:::
Db      438 AsnAlaLeuAlaPheAlaValGlyArgThrAlaProGluMetArgSerLysAlaPheAsn 457
      |||||::: |||||::: |||||::: |||||::: |||||:::
Qy      754 -----CTGCCAGCGTGGCCACCGCCTGCAC 780
      |||||::: |||||::: |||||::: |||||::: |||||:::
Db      458 ThrAlaIleGluAsnIleSerAlaAsnLeuProLeuProSerPhePheTyGlnAsnHis 477
      |||||::: |||||::: |||||::: |||||::: |||||:::
Qy      781 -----GAGAGCGCTGGAGCGCGCCCGCCATGTTCCCGCCACCTTC 822
      |||||::: |||||::: |||||::: |||||::: |||||:::
Db      478 HisTrpArgIleTyTyArgAspAspGlnLeuProLysHisThrGlnPheAsnAspGluTy 497
      |||||::: |||||::: |||||::: |||||::: |||||:::
Qy      823 CTGTACACGCGAGCTGTGGAGGACCCCGAGCCGATATGGAGGTGATGGAGATCAACCCC 882
      |||||::: |||||::: |||||::: |||||::: |||||:::
Db      498 IleTyAlaPheThrTrpGluAspSerArgValAspArgGluLeuLeuAsnLeuGlyPro 517
      |||||::: |||||::: |||||::: |||||::: |||||:::
Qy      883 AAGGACACGGTGTGCTGACCTGACTAGCGGCGGTGCAATGCCCTGAACTGCTGCTGCGAG 942
      |||||::: |||||::: |||||::: |||||::: |||||:::
Db      518 AspAspValValLeuAlaIleThrSerAlaGlyAspAsnIleLeuSerTyLeuMetGln 537
      |||||::: |||||::: |||||::: |||||::: |||||:::
Qy      943 GGGGCCGCGCAGGTGTGCTGCTGGAGCTGCAACCCCGCGAGCTGGCGCTTCTGGAGCTG 1002
      |||||::: |||||::: |||||::: |||||::: |||||:::
Db      538 SerProAlaArgValHisAlaIleAspLeuAsnProAlaGlnAsnHisLeuLeuGluLeu 557
      |||||::: |||||::: |||||::: |||||::: |||||:::
Qy      1003 AAGAAGGTGGCCATTACGACGCTGGAGCTTTGAGGACGCTGGAGCTGTTCCGGCGAGGGC 1062
      |||||::: |||||::: |||||::: |||||::: |||||:::
Db      558 LysValAlaSerPheThrThrLeuAspTyProAspValTrpLysIlePheGlyGluGly 577
      |||||::: |||||::: |||||::: |||||::: |||||:::
Qy      1063 GTGCACCGCGCATTTAGAGAGCTGTACGAGAAGCTGGCGCCCTCTCTGTTCGCAACCC 1122
      |||||::: |||||::: |||||::: |||||::: |||||:::
Db      578 LysHisProAspPheArgSerLeuLeuLeuSerLysLeuSerProHisLeuSerGlyArg 597
      |||||::: |||||::: |||||::: |||||::: |||||:::
Qy      1123 AGCCAACTTCTGTGTCCAAGCGCTCTGTGATCTTCCAG-----CACGGCGCTG 1170
      |||||::: |||||::: |||||::: |||||::: |||||:::
Db      598 AlaPheGlnTyTrpLeuSerAsnAlaHisIlePheThrAspProAlaGlyArgGlyLeu 617
      |||||::: |||||::: |||||::: |||||::: |||||:::
Qy      1171 TACTACACGCGCGCATGGCCAGCTGTGCTGGGTGTGCTGCTGCGCTGGCGGTGTGCTG 1230
      |||||::: |||||::: |||||::: |||||::: |||||:::
Db      618 TyrAspThrGlyGlySerArgTyAlaIleArgPhePheArgTrpIleSerThrLeuPhe 637
      |||||::: |||||::: |||||::: |||||::: |||||:::
Qy      1231 GGACTGGCGCAAGACCGCTCAAGCGCTCGCCCAACCGCCCAATGGAGGACGACGCGGT 1290
      |||||::: |||||::: |||||::: |||||::: |||||:::
Db      638 PheCysArgSerAlaValArgValArgLeuSerThrProThrLeuGluGlyGlnArgSer 657
      |||||::: |||||::: |||||::: |||||::: |||||:::
Qy      1291 CTGTGGGACGACCAATGCTCATCTTCATCGTGAAGAACGGGCCCAAGCCGCTGTGTGG 1350
      |||||::: |||||::: |||||::: |||||::: |||||:::
Db      658 IleTyHisThrIle-----ArgProCys----- 666
      |||||::: |||||::: |||||::: |||||::: |||||:::

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Qy	1351	CTGTTCTCAAGTTCGTGACG---CTGGTGCTCTTCAACAAGCGGTGCTGTGTTCCGC	1407
Ds	667	LeuLeuAsnArgPheValAsnGlyLeuValLeuSerSerAspAlaPheLeuTrpSerAla	686
Qy	1408	GCGCGCTGCCGGCAAGCAGTCGCTGATCAAGCGGAC-----	1449
Ds	687	LeuGlyValProLysAsnGlnValAlaMetIleGlulaAspTyrHisArgArgSerIle	706
Qy	1450	-----GGCATCCCATTTAGAACC	1467
Ds	707	SerSerSerThrThrProSerSerLysGluLysProSerArgAlaGluAlaIleLeuHis	726
Qy	1468	TACATCGCGCACCATGGACGGGTGGCGAGAACTCGCACGTGGCGCAACGAACTAC	1527
Ds	727	TyrThrThrSerThrLeuAspProValLeuSerThrSerHisLeuAlaSerAspAsnPro	746
Qy	1528	TTCTACTACAACTGCCTCACCGCAAGTCTCTGCGCAACAACCTGCCCACTACTCTCGC	1587
Ds	747	TyrTyrlieuValCysValLeuGlyGlnTyrThrArgGlnCysHisProAspTyrLeuSer	766
Qy	1588	GAGCGCGCTTCGCCACCTCAAAGAT---GGCTGTGTGGACAACCTGACGGTCTCCACC	1644
Ds	767	ProAlaAlaHisSerIleLeuSerAlaAspProGlyAlaPheAspGlyLeuArlleHisThr	786
Qy	1645	AAC TTCTTCATGGAGGAGCTC-----AAACGGCGCACTACACCAAGGTGATTCTG	1695
Ds	787	AspGluIleGlnGluValLeuAlaArgPheGlnProGlyThrLeuThrValAlaValAla	806
Qy	1696	ATGACACCACTGGACTGGCTGGATATGCC-----	1725
Ds	807	MetAspSerMetAspTrpPheAspProSerProGluGluGluLysGluGlyArgGly	826
Qy	1726	GTGCCCCAACGAGCTGGCGGAGTGCTCTGGCCAAGCAGAGTTCGCGCGGGCGGATCGTCATC	1785
Ds	827	LysAlaArgGluGlnValArgArgLeuAsnArgAlaLeuLysValGlyGlyLysValLeu	846
Qy	1786	TGGCGCTCCGCTCCCTCCAGCCCGCTACGCGAGCTGATCCAGAGGGCGGCTTCGAC	1845
Ds	847	LeuArgSerAlaGlyValGluProTrpTyrValArgValPheValGluGluGlyPheGly	866
Qy	1846	GTGCGCTGCATC-----CGCGCGCCCACTCAGGCGCTACATGGACCGCGCTC	1890
Ds	867	AlaArgArgValGlyCysArgGluSerGlyArgGlyAspGlnGluCysIleAspArgVal	886
Qy	1891	AACATGTACAGCTCTCTTCTACATGGCCCGCGCG	1923
Ds	887	AsnMetTyrAlaSerCysTrpIleLeuGluLys	897

RESULT 4

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US-10-084-846A-6
; Sequence 6, Application US/10084846A
; Publication No. US2004006026A1
; GENERAL INFORMATION:
; APPLICANT: WEITNAUER, GABRIELE
; APPLICANT: MUHLENWEG, AGNES
; APPLICANT: TREFFZER, AXEL
; APPLICANT: BECHTHOLD, ANDREAS
; TITLE OF INVENTION: AVILAMYCIN DERIVATIVES
; FILE REFERENCE: 1974-005
; CURRENT APPLICATION NUMBER: US/10/084,846A
; CURRENT FILING DATE: 2003-02-25
; PRIOR FILING DATE: 2001-08-24
; PRIOR FILING DATE: 2001-08-24
; PRIOR FILING DATE: 2001-08-24
; PRIOR FILING DATE: 2001-02-25
; NUMBER OF SEQ ID NOS: 120
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 6
; LENGTH: 19662
; TYPE: PRT
; ORGANISM: Streptomyces viridochromogenes
; FEATURE:

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QY 1270 TGGCGCGCTTGGCGAGCGCTTGAGCGTCTGCCCGTCCAGCACCAGCCAGGCACT 1211
Db 12655 TrpGlyArgValAlaSerProAlaArgSerAlaAlaArgAlaProArgAlaProGlyAsn 12674
QY 1210 GCAGCA-----CCC 1202
Db 12675 AlaAlaProAlaThrAspProArgThrThrProArgProArgProArgArgPro 12694
QY 1201 AGCAGCTTCCCATGCGCG-----CCTGTAGTACAGCGCGTCTGGGA 1157
Db 12695 AlaArgArgCysProAlaAlaArgProAlaAlaArgProGlySerAlaGlyArgAlaGly 12714
QY 1156 AGTACCAGAGCGCT----- 1142
Db 12715 SerProGlyValProProArgProProGlyArgAlaArgCysArgArgGlyAsp 12734
QY 1141 -----TGG 1139
Db 12735 ArgAlaArgProArgProSerProProValAlaCysArgArgArgSerArgArg 12754
QY 1138 ACCAGAGTTGGCTGGTT-----GCCAGGGAAG 1106
Db 12755 AlaArgProCysGlyAlaAlaGlyGlyProArgArgProAlaAlaArgSerThrSerArg 12774
QY 1105 GCGCAGCTTCTCT---CGTACA-----GCTCCTCAATGCGCGGTGCA 1064
Db 12775 ArgProAlaAlaGlyProArgThrArgArgAlaAlaArgAlaProGluArgAlaValHis 12794
QY 1063 CGCCCTCGCCGAACAGCTGCG-----ACACGTCTCTCAA 1031
Db 12795 ArgAspArgArgThrValAlaAlaArgSerAsnArgAsnArgSerArgValArgProPro 12814
QY 1030 ACTCAGCTGCTGAATGCCACCTTCTTACAGCTCAGAGCGCGACTGCGCG---GGT 974
Db 12815 ArgProAlaAlaGlyArgProGlyArgGlyArgProValArgAlaGlyAlaArgProGly 12834
QY 973 TGCAGTCCACGACACCACTGCGCG-----CCCCCTGACAGCAGGTTTCAGGCGAT 920
Db 12835 ProAlaAlaThrAlaProProAspArgArgGlyProAlaAlaArgProSerGlyProArgHis 12854
QY 919 ---TGCAGCCCGCTAGTCAGG---TCAGCACCGTCTCTTGGGGTGTGATCTCCATCA 866
Db 12855 GlyArgAlaAlaArgGlySerGlyArgArgArgProArgProSerGlyArgProAlaAla 12874
QY 865 CCTCATATCCGGCTCGGGTCTCTCCACGACTCGGTGTACAGAAAGTGGCGCGGAACA 806
Db 12875 ProProArgPro---ArgGlyArgPro-----GlySer 12884
QY 805 TGGGCGCGCTCCACGCGCTCTCGTCAGGGCGTGCCCAACGCTGGGCAAGCGCCAA 746
Db 12885 AlaAlaAlaProProSerAlaPro-----GlyGlySer 12895
QY 745 TCCACAGCTAGTGGGGCGCGCAGCCACGACGCTAGGGATCGAACCTGGGTGTCT 686
Db 12895 SerSerCysProGlyGlyArgGlyAlaLeuArgProArgArgArgProProGly---Thr 12914
QY 685 GCTCCACACGCGCTCCAGCTTCTGCTCCAGGTAGG---CGCGGCTCGGGC----- 635
Db 12915 ProProAlaAlaArgProGlyArgSerProArgArgGlyArgGlyCysProGlyThrGly 12934
QY 634 -----CGATGTCATGTTGT-----CGATGT-----CGAAGA 608
Db 12935 GlyCysArgArgProAlaCysGlyAlaThrAlaAlaThrAlaAlaGlyArgCysProArgArgArg 12954
QY 607 TCGATC-----GCCAGAGAAACGCGCGCACAGG----- 578
Db 12955 AlaCysProAlaAlaCysGlySerArgArgArgGlyArgAlaAlaArgProLeuAlaProArg 12974
QY 577 -----GCATCTGGCGGCGCGCGAGGTCTGATTTC----- 548
Db 12975 ArgTrpAsnAlaThrAlaGlyGlyAlaAlaAlaAlaAlaAlaAlaGlyLeuArgGlySer 12994

QY 547 -----CGCTCAGCTAGAAAGTCGGCAACCGCCACCGCCAGGC 515
Db 12995 ArgSerAlaGlyAlaProThrSerProArgSerArgArgGlySerGlyArgArgProArg 13014
QY 514 CGTCTTGGGACAGGTACAGCAAGCCTGTGCGATGACGTTGT-----GGAAACGTTGAA 461
Db 13015 ArgArgGlyArgSerGlyProArgAlaGly-----CysAlaValAlaSerValArg 13031
QY 460 TCATCGTGCGGAGTAGAGAGAGGTGATGAGCGTCCGG-----TGCCCTCAG 413
Db 13032 ArgThrArgProProArgArgValArgProAlaSerArgGlySerSerAlaArgProArg 13051
QY 412 GGGCGCAAAATTGGCAAGCGTCGCGCT-----CCACACCTGACCATTTCT--- 368
Db 13052 GlyAlaGlyThrAlaAlaArgThrProGlyGlyArgProArgProArgSerArg 13071
QY 367 -----TCCAGCGCTTGG 356
Db 13072 ArgAlaAlaProGlyCysAlaGlySerProProSerThrArgArgArgSerProTrp 13091
QY 355 CCT-----TCGCGCTTCT-----TCTTGSCCA----- 335
Db 13092 ProAlaGlyProArgAlaProSerCysArgAlaAlaCysAlaValArgTrpAspSerAla 13111
QY 334 -----CCTCGCACAGCG-----AGTGGCACAGGTTCGACCA 305
Db 13112 ArgArgArgProArgAlaAlaGlyArgAlaGlyGlyProCysAlaGlyCysGlyArgPro 13131
QY 304 CGT----- 302
Db 13132 ArgArgArgProAlaValArgProAlaProArgArgSerSerGlyArgArgProSer 13151
QY 301 -----AGATGGACTTGAAGTTCGCGCGCGTGCATGTAAT 269
Db 13152 ArgProArgArgGlyHisArgArgSerArgTrpThr---SerSerArgThrArgTrpPro 13170
QY 268 CAGCCATCATATCAGCATTTCTCCCGAGTGC----- 239
Db 13171 ArgProPro---ArgHisCysProArgAlaAlaAlaArgArgProArgArgAlaAspPro 13189
QY 238 -----CACCAACCGGTCAACCCAGATGAGTTCCGAGC-----GCTCGCGCCAGGC 194
Db 13190 SerProSerArgHisAlaProArgProArgProArgAlaAlaAlaThrTyArgSerAla 13209
QY 193 GGGCAGCAAGGAGCGCGCTGGGGCGCGTAGAAGCTCTCCAGCGCAGCAGCGTATCAT 134
Db 13210 GlyProArgArgSerArgSerAlaProArgArg-----ArgArgArgSerHis 13226
QY 133 CGCCCTTCT-----TGTGCCGAACCCACA 110
Db 13227 ArgProSerGlyArgArgArgAlaAlaArgProValThrAlaThrAlaArgAla 13246
QY 109 TATGGCGCAGAACGG-----TCAGGT-----CATCTTCATGCTGCTGAGCTTGA 65
Db 13247 ArgAlaAlaSerArgArgSerTrpSerGlyArgArgArgProArgCys----- 13262
QY 64 GCTTCTCCAGGAGAAAGTTCTTCTGTGTAGTCTCGCAGCGCGCGCTCACGACCCGACC 5
Db 13263 -----GlyArgProProAlaAlaSerAlaGlyAlaArgThrArgSerProProThr 13279
QY 4 CCA 2
Db 13280 Pro 13280
RESULT 5
US-10-084-846A-5
; Sequence 5, Application US/10084846A
; Publication No. US20040006026A1
; GENERAL INFORMATION:
; APPLICANT: WEITNAUER, GABRIELE
; APPLICANT: MUHLENWEG, AGNES
; APPLICANT: TREFFER, AXEL
; APPLICANT: BECHTHOLD, ANDREAS

; TITLE OF INVENTION: AVILAMYCIN DERIVATIVES
 ; FILE REFERENCE: 1974-005
 ; CURRENT APPLICATION NUMBER: US/10/084,846A
 ; CURRENT FILING DATE: 2003-02-25
 ; PRIOR APPLICATION NUMBER: PCT/EP01/09815
 ; PRIOR FILING DATE: 2001-08-24
 ; PRIOR APPLICATION NUMBER: DE 101 09 166.4
 ; PRIOR FILING DATE: 2001-02-25
 ; NUMBER OF SEQ ID NOS: 120
 ; SOFTWARE: PatentIn Ver. 3.2
 ; SEQ ID NO 5
 ; LENGTH: 19723
 ; TYPE: PRT
 ; ORGANISM: Streptomyces viridochromogenes
 ; FEATURE:
 ; OTHER INFORMATION: Protein 3: amino acid sequence encoded by coding strand 1.
 ; OTHER INFORMATION: Start codon: atc, Start position: nucleotide 3.
 US-10-084-846A-5

Alignment Scores:

Pred. No.:	1,95e-19	Length:	19723
Score:	459.00	Matches:	241
Percent Similarity:	30.8%	Conservative:	48
Best Local Similarity:	25.7%	Mismatches:	271
Query Match:	12.7%	Indels:	378
DB:	4	Gaps:	50

US-10-620-914-44 (1-1947) x US-10-084-846A-5 (1-19723)

QY	32	GCTACACCAAGAAGAACTTCTCCCTGGAGAGACTCAAGCTCAGCAGCATGAAGATGACC	91
Db	6473	AlaArgProGlyValAlaArgTrpArgTrpSer	6484
QY	92	TCACCGTTCTCGCCCATATGTGGTTTCG	
Db	6485	-----ValCysProSerThrArgProProSerGlySerArgAlaMet----	6498
QY	140	ACGCTGCTCGCTGAGAGCTTCTACGGGCCCCAGG	
Db	6499	-----ThrArgTrpSerArgProSerArgProArgArgProProSerProValThr	6516
QY	191	CCCGCTGGCCGAGCGCTCGAACCTCATCTGGGTGACCTGGGTGGGCTGGGAGGA	250
Db	6517	ProAlaArgSerArgSerSerAlaAlaGlyProThrArgGlyTrpSerTyrGlyGly	6536
QY	251	ATGTCGATATGATGGCTGATTACATCGACCTGGCGAAGTTCAAAGTCCATCTACGTGGTCG	310
Db	6537	Ser-----ProProThrTrpProSerThrAla---ArgThrTrpThr	6549
QY	311	ACCTGTGCACTCGCTGTGCGAGGTGGCCA	340
Db	6550	ProCysSerThrGlyCysAlaArgProProThrSerValProAlaHisArgThrArgArg	6569
QY	341	-----AGAACAGCGGAGCCAGGCTGGAGA-----ATGTCAGGTCTGGAGG	388
Db	6570	SerThrArgArgSerArgThrArgGlyProArgProProThrAlaArgThrGlyArg	6589
QY	389	CCGACGCTTGCCAAATTG-----CGCCCTGAGGGCAGCGCAGCTCATCCTCTCT	442
Db	6590	ArgThrCysAlaThrArgCysGlySerProProArgSerProArgSerProArgThrAla	6609
QY	443	CCTACTCGCTCAGCATGATTCACCGTTCCACACGTCATCGACCGAGCTTGCTCGTACC	502
Db	6610	ThrGlyArgSerSerCysProArgThrProTrpSerArgThrArgSerThrArgArg	6629
QY	503	TGTCCTCAAGACGGCTCG-----	520
Db	6630	TrpProAlaAlaAlaTrpArgThrCysSerSerAspArgArgTyrGlyAlaThrSerPro	6649
QY	521	-----TGGCGTTGCGGCTTCTACGTGAGCG-----	547
Db	6650	ArgProGlyProSerAlaProProTrpAlaProProThrAlaThrAlaAlaTrpThrGly	6669

QY	548	-----GCAAGTACGACCTGCCCCCTGCGCCAGATGCCCCCTGCTGCGCCCGCTT	592
Db	6670	ArgArgSerSerArgThrGlyThrSerLysSerCysArgProThrProGlySerThrAla	6689
QY	593	TCTTCTGCG-----GATCGATCTTCGACATCGACACATTCGACATTCGACATCG	634
Db	6690	ArgCysGlyValProSerProGlyArgGluArgProSerAlaAlaThrThrSerThr---	6708
QY	635	CCCCGAGCGCGCCCTACCTGAGCAGAGAGCTGGAGCGGTGTGGAGCAGAGAACCC	694
Db	6709	-----ProThr-----ArgCysTrpAlaArgProAla	6717
QY	695	AGGTTTCGATCCCTACGTGCGGTGGTGGCGGCCCTACTACTGCTGTGGATTGGCCGC	754
Db	6718	AlaSerArgAlaAlaThrCys---GlyCysGlyThrAlaArgTrpThrThrAlaAla	6736
QY	755	TGCCAGCGTTGGCCACGCCCTCGACGAGDAGCGGTGGAGCGCGGCCCTGTTCCCGC	814
Db	6737	ArgThrArgAlaAlaThrProSerThr-----AlaTrpArgSer-----SerArg	6751
QY	815	CCACCTTCTCTACACGCGAGTCTGGGAGdACCCCGACCGGATATGGAGGTGATGGAGA	874
Db	6752	ProPro---CysTrpArgSerArgSer-----TrpArg	6761
QY	875	TCAACCCCAAGCACACGGTGTGACCTGACTAGCGCGGTGCATGCCCTGAACTGCC	934
Db	6762	ProAlaProArgAlaLysSer-----AlaAlaProSerArgThrArgProThr	6777
QY	935	TGGTGCAGG-----GGCCCGCCAGGTGTGTCGGTGG	967
Db	6778	ArgCysArgArgValSerGlySerArgSerSerAlaAlaArgAlaArgTrpCysGlyTrp	6797
QY	968	-----ACTGCAACCCCG-----	979
Db	6798	ProProGlyArgSerArgThrProProThrArgThrProProGlySerSerMetProArg	6817
QY	980	-----CGCAGTCGCGCG-----	991
Db	6818	ProGlyArgProArgArgThrSerProValTrpArgArgGlyArgCysTrpThrArgAla	6837
QY	992	-----TTCTGGAGCTCAAGAGGTGGCCATTGACGACG	1024
Db	6838	SerThrGlySerAsnArgProThrProAlaTrpSerProGlyGlyTrpPro-----Arg	6855
QY	1025	TGGAGTTTGAGAGCGTGTGGCAGCTGTTdCGCAGAGCGG---TGCACCCGCGCATTTAGG	1081
Db	6856	TrpAlaTrpProArgProValSerIleGlyAlaSerSerAspCysProProValSerVal	6875
QY	1082	AGCTGTACGAGAGAAGCTGGCGCCCTTCTGTGCGAAACCCAGCCACAACTTCTGGTCCA	1141
Db	6876	TyrCysThrLeuArg-----CysSerArgProThrProArgProGlyPro	6890
QY	1142	AGCGCTCTGCTACTTCCAGCAGCGCTGTACTACCAGG-----GCGGCATGGCAGC	1195
Db	6891	ArgCys-----TrpThrProCysArgSerArgArgProProSerTrpAlaSer	6906
QY	1196	TGTCTGGTGTGCTGCTGCTGCGCTGTGTGCTGGGACTGGGCAAGACCGCTCAAGC---	1252
Db	6907	ArgSer-----SerAlaTrpSer---CysThrSerThrArgSerProSerThrAla	6922
QY	1253	-----GCTCGCCCAAGC-----	1264
Db	6923	ArgHisArgArgArgArgSerArgSerIleProAlaSerProThrProCys	6942
QY	1265	-----CGCCCAATGGAGGACGCGCGCTGTGGGACA	1300
Db	6943	ThrProTrpSerArgThrGlyArgAspAlaArgTrpArgAlaCysAlaAlaCysAlaThr	6962
QY	1301	GCAACATGCTCATCCATCTCGTGAAGAACCGGCCCAAGCCGC-----	1342
Db	6963	ArgTrpSerSerArgProArgArgThrProThrSerArgAlaAlaThrArgThrArg	6982
QY	1343	---TGGTGT-----GGCTGTGTCG-----	1357

6983	Db	ThrTrpCysArgSerArgValCysArgArgSerCysValProGlyCysSerThrArg	7002
1358	Qy	-----TCAAGTTTCGTGAGCTGGTGTCTTCA-----ACAAGGCGTGCTGT-----	1399
7003	Db	CysAlaSerArgSerArgArgCysAspSerProProArgProCysThrPheAlaAla	7022
1400	Qy	-----GGTTCCGCGCGCGTCCCGGCAAGC	1426
7023	Db	ArgTrpTrpSerArgGlySerThrArgArgTrpTrpSerAlaAlaGlyTrpArgSerAla	7042
1427	Qy	AGTACGGCGTGATCAAGCGGAGCGCATCC-----CCATTGAGAAGTACATCG	1474
7043	Db	SerAlaGlyThrCysArgProThrSerSerGlySerCysProProSerAlaThrSerSer	7062
1475	Qy	CGCGCACCA-----TGGACGGCGTGGCGGAGAACTCGCAGTCGCGCAAGCAGAACT	1525
7063	Db	IleThrProAsnAlaSerArgAsnThrArgArgArgThrAlaMetArgProGluArgThr	7082
1526	Qy	ACTTCTACTACACTGCCTCACCGGCAAGTTCCTGCGCGCAAACTGCCCACT-----	1579
7083	Db	AspSerValThrHisValSerArgGlyArgGlyGluArgAlaAlaProAlaGlyPro	7102
1580	Qy	-----ACCTGCGGAGGCGCGCTTCGCCA	1603
7103	Db	GluThrGlyLysProGluLysHisAlaSerThrIleValValGlyArgArgHisSerMet	7122
1604	Qy	CCCTCA-----	1609
7123	Db	ProSerGlyValProLeuLysArgProAspLeuThrAlaLeuThrAlaArgCysGlyIle	7142
1610	Qy	---AGAGTGGCGTGGTGGCAAACTGACCGTCTCCACCACTTCTTCATCGAGGAGCTCA	1666
7143	Db	ArgArgSerTyrtTpTp-----AlaGlyLeuAlaArgGlyCys	7155
1667	Qy	AAGCGCGCACTACACAAGGTGATTCGTGATGACACACGTGG-----	1708
7156	Db	GlyArgLeuArgIleProArgProAsnAsnTrpSerArgTrpProIleGluLeuPheSer	7175
1709	Qy	---ACTGGCTGGATA-----	1720
7176	Db	ProMetTyrtTpIleProSerArgArgProGluTytrArgArgSerGlyLeuSerSerGly	7195
1721	Qy	-----TGCCCGTGCCCAACGAGCTGGCGAGTGCCTCGCCCAAGC	1759
7196	Db	ArgProArgArgSerArgLeuProTrpGluThrAlaArgSerSerAlaTrpThrSer	7215
1760	Qy	AGTTGGCGCGGGCGGATCGTCATCTGGCGCTCCGCTCCCTCAGCCCGCCCTACGCCG	1819
7216	Db	ProThrSerSerArgThrProArgAlaGlyTrpProThrProCysSerCysProValThr	7235
1820	Qy	AGCTGATCCAGAAGCGGGCTTCGACCTGC-----	1849
7236	Db	Ser---SerAlaThrThrThrSerSerCysThrTrpAlaThrThrThrSerTrpThrAla	7254
1850	Qy	-----GCTGCATCCGCGCGCCACTCAGG-----	1873
7255	Db	SerSerThrSerTrpArgThrSerAlaAlaThrSerProProArgArgSerCysSerPro	7274
1873	Qy	-----	1873
7275	Db	GlySerProThrArgAlaGlySerAlaTrpProAsnLeuThrArgThrAlaGlyProArg	7294
1874	Qy	-----GCTACATGGACCGGTCAACATGTACA-----	1900
7295	Db	SerTrpArgSerProArgThrProGlyAlaThrTrpArgSerSerAlaCysThrProSer	7314
1901	Qy	---GCTCCTCTTACA-----TGCCCGCGCGGAAGGGCGGCAAGAGCAACT	1945
7315	Db	AlaArgProCysThrArgProTtpProAlaSerGlyArgProGlyGlyThrSer	7332

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; Sequence 5, Application US/10084846A
; Publication No. US20040006026A1
; GENERAL INFORMATION:
; APPLICANT: WEITNAUER, GABRIELE
; APPLICANT: MUHNWEG, AGNES
; APPLICANT: TREFFZER, AXEL
; APPLICANT: BECHTHOLD, ANDREAS
; TITLE OF INVENTION: AVILAMYCIN DERIVATIVES
; FILE REFERENCE: 1974-005
; CURRENT APPLICATION NUMBER: US/10/084,846A
; CURRENT FILING DATE: 2003-02-25
; PRIOR APPLICATION NUMBER: PCT/EP01/09815
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: DE 101 09 166.4
; PRIOR FILING DATE: 2001-02-25
; NUMBER OF SEQ ID NOS: 120
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 5
; LENGTH: 19723
; TYPE: PRT
; ORGANISM: Streptomyces viridochromogenes
; FEATURE:
; OTHER INFORMATION: Protein 3: amino acid sequence encoded by coding strand 1.
; OTHER INFORMATION: Start codon: atc, Start position: nucleotide 3.
US-10-084-846A-5

Alignment Scores:
Pred. No.: 2,41e-19 Length: 19723
Score: 457.50 Matches: 242
Percent Similarity: 33.1% Conservative: 46
Best Local Similarity: 27.8% Mismatches: 256
Query Match: 12.6% Indels: 325
DB: 4 Gaps: 55

US-10-620-914-44 (1-1947) x US-10-084-846A-5 (1-19723)
Qy 1945 AGTTGTCTCTTCGGCGCCCTTCGGCGGCATGTAGA----- 1907
Db 6222 SerThrSerGlyTyrArgPro-----GlyProCysArgGlyProSerValArgThrPro 6239
Qy 1906 -----AGGAGCTGTACATGTTGACGGGTCCATGTAGC-----CCT 1871
Db 6240 AlaGlyArgLeuCys-----ProValSerAlaThrAlaAlaProTrpPro 6254
Qy 1870 GAGTGGCGCGCGGATGACGGCAGTCGCGAGCGCCTCTGGATCAGTCCAGTGGTCCATCAGAA 1811
Db 6255 MetTrp-----SerSerAsnArgArgProProArgProProAlaProArgArg 6270
Qy 1810 GCGGGCTGAGGGAGCGGAGCCAGATGACGATGCCCGCGCCAACTCTGTGGCCA 1751
Db 6271 Ser-----ArgPro---GluProCysSerArg 6278
Qy 1750 GGCACTGGCGAGCTGTTGGCCACGGGCATATCAGCCAGTCCAGTGGTCCATCAGAA 1691
Db 6279 CysProArgProProArg---ArgArgSerValThrAlaArgProArgSerProSerGly 6297
Qy 1690 TCACCTGGTGTAGTGGCGCTTTGACCTCTCCATGAAGAAGTTGGTGGAGACGGTCA 1631
Db 6298 Ser-----ArgArgAlaLeu-----ThrTrpProArgSer 6307
Qy 1630 GGTGTGCCA-----CCAGCCACTCTTGAGGG-----TGCGCAAGG 1595
Db 6308 GlyThrProTrpProLeGlySerProArgTrpSerThrGlyArgProSerTrpArgPro 6327
Qy 1594 -----CGCCCTCGGCAGGTAGGTGGGC----- 1571
Db 6328 AlaGlyThrAsnTrpProProGlyCysAlaArgTrpProLeuArgAsnProArgProVal 6347
Qy 1570 AGTTGTGCGCGCAGGAACTTGCGGGTGAGCGAGTGTGTAGTAGAAGTAGTTCTGCTCGCA 1511
Db 6348 SerSerProGlyProArgCysArg-----MetProAlaValProSerGlyCysSer 6364
Qy 1510 CGTGCAGTCTTCGGCCACGCGGTCCATGTTGTCGCGCATGT----- 1469

```

Db 6365 ArgValThrGlyProSerGlyProGlyTrpAlaAlaAenCysTrpLysProSerArgSer 6384
||| :||| ||| ||| ||| |||
Qy 1468 -----AGTTCTCAATGG-----GATGCGGTCGCGCT 1442
||| :||| ||| ||| ||| |||
Db 6395 SerProArgSerThrAsnTrpSerArgCysSerArgArgArgSerGlySerArgPro-- 6403
||| :||| ||| ||| ||| |||
Qy 1441 TGATCAGCGGTACTGCTGCGCGCAGCGCGCGCCGAAACACAGCA---CGGCTTGT 1385
||| :||| ||| ||| ||| |||
Db 6404 -----GlyArgCysCysTrpArgAlaThrThrProArgSerThrAlaProArgProSer 6421
||| :||| ||| ||| ||| |||
Qy 1384 TGAAGAGCACCA-----GGCTCAGCAACTTGACGAACACGACACCA 1343
||| :||| ||| ||| ||| |||
Db 6422 SerArgCysSerSerGlySerProArgCysGlyGlyHisGlyAlaSerSerProPro 6441
||| :||| ||| ||| ||| |||
Qy 1342 CGGCTTGGCGCGTCTTTCAGAGT----- 1316
:||||| ||| ||| ||| ||| |||
Db 6442 SerSerAlaThrArgSerValArgSerProProSerProProGlyArgProProThr 6461
||| :||| ||| ||| ||| |||
Qy 1315 -----GGATGAGCA-----TGTGCTGTCCACAGAGCGGCTGCTCCTCCATTG 1271
||| :||| ||| ||| ||| |||
Db 6462 GlyProGlySerAlaValGlyArgCysCys-----AlaArgProArgGly 6477
||| :||| ||| ||| ||| |||
Qy 1270 TGGGCGGCTTGGCGAGCGCTGAGCGTCTGCCAGTCCAGCACCA----- 1223
||| :||| ||| ||| ||| |||
Db 6478 ValAlaArgTrpArgTrpSer-----ValCysProSerThrArgProProSerGlySer 6495
||| :||| ||| ||| ||| |||
Qy 1222 -----CGGCCAGGCACTGCAGCACCCAGCACAGCT 1193
||| :||| ||| ||| ||| |||
Db 6496 ArgAlaMetThrArgTrpSerArgProSerArgProArgArgArgProProSerProVal 6515
||| :||| ||| ||| ||| |||
Qy 1192 TGCCCATGCGCCCTGTGTACAGCGCTGTGAAGTACAGAGCGGCTGTGACACAGA 1133
||| :||| ||| ||| ||| |||
Db 6516 ThrProAlaArgSerArgSerSerAlaAlaGlyProThrArgGly---TrpSerTyr 6534
||| :||| ||| ||| ||| |||
Qy 1132 AGTTGTGGC-----TGCTTTCGACAGGAAG----- 1106
||| :||| ||| ||| ||| |||
Db 6535 GlyGlySerProProThrTrpProSerThrAlaArgThrTrpThrProCysSerThrGly 6554
||| :||| ||| ||| ||| |||
Qy 1105 -----CGGCCAGCT-----TCTTCTCGTACAGCT 1082
||| :||| ||| ||| ||| |||
Db 6555 CysAlaArgProProThrSerValProAlaHisArgThrArgArgSerThrArgArgArg 6574
||| :||| ||| ||| ||| |||
Qy 1081 CCTCAATGCGCGGTGACAGCGCT-----CGCCGAACAGCTGCCACA 1040
||| :||| ||| ||| ||| |||
Db 6575 SerArgThrArgGlyProArgProProThrAlaArgThrGlyArgArgThrCysAlaThr 6594
||| :||| ||| ||| ||| |||
Qy 1039 CGT-----CCTCAACTCCA-----GCTGCTGAATGCCCACTTCT 1004
||| :||| ||| ||| ||| |||
Db 6595 ArgCysGlySerProProArgSerProArgArgProArgThrAlaThrGlyArgSerSer 6614
||| :||| ||| ||| ||| |||
Qy 1003 TCAGCTCCAGAAAGCGCCGACTGCG----- 980
||| :||| ||| ||| ||| |||
Db 6615 SerCysProArgThrProTrpSerArgThrArgSerThrArgArgTrpProAsnAlaAla 6634
||| :||| ||| ||| ||| |||
Qy 979 ---CGGGTTCAGT-----CCACCG 962
||| :||| ||| ||| ||| |||
Db 6635 TrpArgThrCysSerSerAspArgArgTyrGlyAlaThrSerProArgProGlyProSer 6654
||| :||| ||| ||| ||| |||
Qy 961 ACACCACTGCGCGGCCCT-----GCACAGAGTTTCAGGGCATTGACGGCGCGC 908
||| :||| ||| ||| ||| |||
Db 6655 AlaProProTrpAlaProProThrAlaThrAlaAlaTrpThrGlyArgArgSerArg 6674
||| :||| ||| ||| ||| |||
Qy 907 TAGTCAGGCTCAGCACCGGTGCTTGGGTTGATCTCCATCACCT----- 863
||| :||| ||| ||| ||| |||
Db 6675 ThrGlyThrSerLysSerCys-----ArgProThrProGlySerThrAlaArg 6690
||| :||| ||| ||| ||| |||
Qy 862 -----CCATATCGCGCTCGGGTCTCTCCACGACTCGGTGTACAGGAAGTGGCGC 812
||| :||| ||| ||| ||| |||
Db 6691 CysGlyValProSerProGlyArgGluArgProSerAlaAlaThrThrSerThrProThr 6710
||| :||| ||| ||| ||| |||
Qy 811 GGAACATGGGG-----GCCGCTCCAGCGCTCTCTGTGTCAGGGCGTGGC---CAAGCG 761
||| :||| ||| ||| ||| |||

RESULT 7

US-10-084-846A-7
; Sequence 7, Application US/10084846A
; Publication No. US2004006026A1
; GENERAL INFORMATION:
; APPLICANT: WEITNAUER, GABRIELE
; APPLICANT: MUHLENWEG, AGNES

Db 6711 ArgCysTrpAlaArgProAlaAlaSerArgAlaAlaThrCysGlyCysGlyThrAlaArg 6730
||| :||| ||| ||| ||| |||
Qy 760 TGGCAGCGCGCCCAATCACACGCTAGTAGGGGCGCGCAGCC-----ACGCGCAGT 710
||| :||| ||| ||| ||| |||
Db 6731 TrpThr-----ThrThrAlaAlaArgThrArgAlaAlaThrProSerThrAlaTrp 6747
||| :||| ||| ||| ||| |||
Qy 709 AGGGATCGAACCTTGGGTCT-----TCTGCTCCACACGCGCT 671
||| :||| ||| ||| ||| |||
Db 6748 ArgSerSerArgProProCysTrpArgSerArgSerTrpArgProAlaPro---ArgAla 6766
||| :||| ||| ||| ||| |||
Qy 670 CCAGCTTCTGCTCCAGGTAGGCGCGCTCGGGCGCATGTCATGTTGTCGATGTCGA 611
||| :||| ||| ||| ||| |||
Db 6767 LysSerAlaAlaPro-----SerArgThrArgProThrArgCysArg 6780
||| :||| ||| ||| ||| |||
Qy 610 AGATCGATCGCAGAAAGAACGCGCGCACGAGCATCTGGCGCAGG-----GCAGGT 557
||| :||| ||| ||| ||| |||
Db 6781 ArgValSerGlyArgSerArgSerSerAlaAlaArgTrpCysGlyTrpProGly 6800
||| :||| ||| ||| ||| |||
Qy 556 GGTACTTGGCGCTCACGTAGNAGTCGGCAACGCCACGCGCGCTCTTGGACACAGGTACG 497
||| :||| ||| ||| ||| |||
Db 6801 ArgSer-----ArgThrProProThrArgThrProProGlySer 6813
||| :||| ||| ||| ||| |||
Qy 496 AGC-----AAGCCTGCTCGATGACGTGTGGAACGCTGGAATCATCTGAGCGAGTAGG 443
||| :||| ||| ||| ||| |||
Db 6814 SerMetProArgProGlyArgProArg-----ArgThrSerProValTrpArg 6829
||| :||| ||| ||| ||| |||
Qy 442 AGAAGGTATGACGCTGCGGTGCCCTCAGGGGCGCAAAATTGCAAGCGCTGCGCCTCCA 383
||| :||| ||| ||| ||| |||
Db 6830 Arg-----GlyArgCysTrpThrArgAlaSerThrGlySerAsnArgPro--- 6844
||| :||| ||| ||| ||| |||
Qy 382 CGACCTCGACATCTTCCAGCCCTTGGCCTTGCCTTCTTCTTGGCCACCTCGCACAGCG 323
||| :||| ||| ||| ||| |||
Db 6845 -----ThrProAlaTrpSerProGlyGlyTrpPro----- 6854
||| :||| ||| ||| ||| |||
Qy 322 AGTGGCACAGCTGCACACGCTAGATGGACTTGAACCTTCCGCCAGGT----- 278
||| :||| ||| ||| ||| |||
Db 6855 -----ArgTrpAlaTrpProArgProValSerIleGlyAlaSer 6867
||| :||| ||| ||| ||| |||
Qy 277 -----CGATGTAATCAGCCATCATATCGA 254
||| :||| ||| ||| ||| |||
Db 6868 SerAspCysProProValSerValTyCysThrLeuArgCysSerArgProThrProArg 6887
||| :||| ||| ||| ||| |||
Qy 253 CATCTCCCGAGTCCACACCCAGGTCAACCCAGATGAGTTTCGAGCGCTCGGCCA--- 197
||| :||| ||| ||| ||| |||
Db 6888 ProGlyProArgCysTrpTrpProCysArgSerArg-----ArgProPro 6902
||| :||| ||| ||| ||| |||
Qy 196 -----GGC 194
||| :||| ||| ||| ||| |||
Db 6903 SerTrpAlaSerArgSerSerAlaTrpSerCysThrSerThrArgSerProSerThrAla 6922
||| :||| ||| ||| ||| |||
Qy 193 GGGCAGCAAGGCGCGCCTGGGGCGCTAGAGCTCTCCAGCGCGAGCAG----- 143
||| :||| ||| ||| ||| |||
Db 6923 ArgHisArgArgArgArgSerArgSerArgSerIleProAlaSerProThrProCys 6942
||| :||| ||| ||| ||| |||
Qy 142 -----CGTGATCATCGCCCTTCTTGTCTGCCGAACACCATATGGC 104
||| :||| ||| ||| ||| |||
Db 6943 ThrProTrpSerArgThrGlyArgAspAlaArgTrpArgAlaCysAlaAlaCysAlaThr 6962
||| :||| ||| ||| ||| |||
Qy 103 GCAGAACGCTCAGCTCATCTTCTATGCTGTGCTGAGCTTTCAGCTTCCAGGAGAGTTCT 44
||| :||| ||| ||| ||| |||
Db 6963 ArgTrpSerSerArgProArgArgThrProThrSerArgAlaAlaThrArgThrArg 6982
||| :||| ||| ||| ||| |||
Qy 43 TCTTGTGTAGTCTGACGCGCGCGCT 17
||| :||| ||| ||| ||| |||
Db 6983 ThrTrpCysArgSerArgValCysArg 6991
||| :||| ||| ||| ||| |||


```

;
; FEATURE:
; OTHER INFORMATION: Protein 3: amino acid sequence encoded by coding strand 1.
; OTHER INFORMATION: Start codon: atc, Start position: nucleotide 3.
US-10-084-846A-8

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QY 992 TTCTGGAGCTGAAGAGGTGGCCATTGAGCAGCTGGAGTTTGGAGACGTGTGGCAGCTGT 1051
Db      :|||
5310 -----AlaAlaArgThrArgSerSerAla 5317
QY 1052 TCGCGGAGG-----GGCTGCACCCGGCGCATTTAGGAGCTGTACGAGAAGAGCTGGCGC 1105
Db      :|||
5318 ThrSerArgSerGlyAlaThrGlyArgAlaAlaArgCysProValArgProGlnGly 5337
QY 1106 CTTCTGCTGCGCAACCGCACAACTTCTGGTCCA-----AGCGCTCTGGT 1153
Db      :|||
5338 AlaSerThrSerSerAlaProArgThrAlaGlyThrGlySerArgCysAlaGlyThrGly 5357
QY 1154 ACTTCCAGCAGCGCTGTACTACGAGCGGCATGGGCAAGCTGTGGTGTGTGCAGT 1213
Db      :|||
5358 ThrAlaSerValSerSerAlaThrArgThrGlySerTrpSerAlaAlaGlyAsnThrPro 5377
QY 1214 GCCTGGCGCTGGTCTGGGAC---TGGGCAAGACCGTCAAGCGCTCGCCAAACGGGCCA 1270
Db      :|||
5378 ThrTrpArgArgCysTrpProArgTrpSerArg-----AsnProArgProCysAlaThr 5395
QY 1371 CAATGGAGGACGCGCGTCTGTGGACAGCAACATGCTCATCCACTTCTGTGAAGAAGC 1330
Db      :|||
5396 SerTrpArgThrAlaSerThrSerArgAlaTyrGlyTrpSerArgThrSer---ProThr 5414
QY 1331 GCGCCAAAGCCGCTGGTGGCTGTTCGTCAGTTGCTGAGCTCG-----TGTCTCTCA 1384
Db      :|||
5415 SerProThrAlaSerThrAlaProAlaThrThrSerProAlaThrProProAlaSerSer 5434
QY 1385 ACAAGGCGCTGCTGTGGTTCGGCGCGCGCTGCGCGGCAAGCAGTACGCGTGTATCAAGG 1444
Db      :|||
5435 ThrArg---CysCysProAlaSerThrTrpArgSerThrAlaAlaCysTrpProArg 5453
QY 1445 CGGACGGCATCCCATTTGAGAACTACATTCGCGGCAACGAGCGGCTGGCGGAGAACT 1504
Db      :|||
5454 ArgProCysSerProArgThrArgThrSerArg-----5464
QY 1505 CGCAGTGGCGCAAGCAGNACTACTTCTACTACACTGCTCACCGGCNAAGTTCCTGGCG 1564
Db      :|||
5465 ArgArgArgProGlyArgSerThrSerArgSerThrAlaThrProThrSerGlyCysSer 5484
QY 1565 ACAACTGCCACCTACCTGCGGAGGCGGCTTCGCCACCTCAAGAGTGGCGTGGTGG 1624
Db      :|||
5485 ProTrpCysProAlaCysThrSerAsnArgProAlaArgProProThrSerSerTrpPro 5504
QY 1625 ACA-----ACCTGACCTCTCCACAACTTCTTCATGAGGAGCTCAAAGCGGCA 1675
Db      :|||
5505 ThrArgProArgSerAlaProArgProSerThrSer-----ArgSerThrAlaArgTrp 5522
QY 1676 CTTACACCAAGGTATCTGATGACCAACGCTGGACTGGCTGGATATGCCGTGGCCCAACG 1735
Db      :|||
5523 ProSerPro-----AsnTrpSerArgAspTrpProThr 5533
QY 1736 AGC---TGGCGGAGTGCCTGCCAAGCAGAGTTGGCGCGGCGCATCG---TCATCTGGC 1789
Db      :|||
5534 SerThrThrProSer-----ProAlaArgThrArgThrAlaProSerArgArgThrPro 5551
QY 1790 GCTCGGCTCCTCAGCGCCGCTACGCCGAGCTGATCC-----1828
Db      :|||
5552 ArgProThrProCysArgArgThrThrProSerAlaSerCysSerArgArgProArgThr 5571
QY 1829 -----AGAAGCGGGCTTCAGAGTGGCTGCATCCGCGCGCCGCGCCACTCAGGCTACATGG 1882
Db      :|||
5572 ProValTrpArgArgProGlyCysProProHisArgSerAlaArgLeuProAlaArgTrp 5591
QY 1883 ACCGGCTCAACATGTACAGCTCCT-----TCTACATGGCGCGCGCGGAAGG 1927
Db      :|||
5592 ThrProThrThrSerThrThrProProArgValSerThrTrpProAlaArgArg 5609
; RESULT 9
; US-10-084-846A-3
; Sequence 3, Application US/10084846A
; Publication No. US2004000626A1
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; GENERAL INFORMATION:

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; APPLICANT: WEITNAUER, GABRIELE
; APPLICANT: MUHLENWEG, AGNES
; APPLICANT: TREFZER, AXEL
; APPLICANT: BECHTHOLD, ANDREAS
; TITLE OF INVENTION: AVILAMYCIN DERIVATIVES
; FILE REFERENCE: 1974-005
; CURRENT APPLICATION NUMBER: US/10/084,846A
; CURRENT FILING DATE: 2003-02-25
; PRIOR APPLICATION NUMBER: PCT/EP01/09815
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: DE 101 09 166.4
; PRIOR FILING DATE: 2001-02-25
; NUMBER OF SEQ ID NOS: 120
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 3
; LENGTH: 19695
; TYPE: PRT
; ORGANISM: Streptomyces viridochromogenes
; FEATURE:
; OTHER INFORMATION: Protein 1: amino acid sequence encoded by coding strand 1.
; OTHER INFORMATION: Start codon: gga, Start position: nucleotide 1.
US-10-084-846A-3
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Alignment Scores:

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Pred. No.: 1,75e-18 Length: 19695
Score: 443.50 Matches: 229
Percent Similarity: 34.3% Conservative: 48
Best Local Similarity: 28.4% Mismatches: 213
Query Match: 12.3% Indels: 317
DB: Gaps: 51
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US-10-620-914-44 (1-1947) x US-10-084-846A-3 (1-19695)

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QY 23 GGCCTGCGAGCTACA-----CCAAGAAGA-----ACTTCTCCTGGAGAGCTCAAGC 70
Db 8455 GlyGluArgArgThrHisProArgArgHisTrpThrGlyProArgArgSerSerGly 8474
QY 71 TCAGCAGCATGAGGATGACCTGACCGCTTCTGCCCATATGCTGTCGGCAGCAAGAGG 130
Db 8475 SerAsp-----GlyThrAlaSerArgThr 8482
QY 131 GCGATGATCACGCTGCTCGCTGGAGAGCTTCTACGGGCCCCAGG-----CCGCTG 181
Db 8483 -----ArgAlaArgPheSerProArgThrArgSerProVal 8494
QY 182 -----CCTTGTGTCGCGCTGGCGAGCGCTCGAACC 214
Db 8495 SerArgArgAlaProAsnGlySerSerProAlaSerProThrArgAlaCysAlaProThr 8514
QY 215 TCATCTGGTTGACCTGGTGGTGGCACTGGGAGATGTCGATATGATGCTGATTACA 274
Db 8515 ThrThrGly-----Thr 8518
QY 275 TCGACCTGGCGAAGTTTCAAGT---CCATCTACGTGGTTCGACCTGTGCCACTCGCTGTGCG 331
Db 8519 SerProSerArgAlaMetSerValProSer-----SerThrAlaCysThr 8533
QY 332 AGGTGGCCAAAGAAAGCGCAAGCGGCTGGAGA-----ATGTCAGGTCTGTGG 385
Db 8534 ThrTrp---ArgSerArgThrGlyProArgAsnGlyThrCysCysThrAlaArgAsnTrp 8552
QY 386 AGGCGGACGCTTGGCAATTTGCGGCCCTGAGGGCACCGGACGCTCATACCTTCTCCT 445
Db 8553 ArgSerSer-----ProProArgSerTrpThrAlaArgSerCysProProPro 8568
QY 446 ACTCGCTCA-----CGATGATTCCACCGTTCCAAACGTC 481
Db 8569 ThrArgSerSerSerArgSerArgThrGlyProArgArgCysHisGlyThrValThrAla 8588
QY 482 TCGACCAAGGCTT---GCTCGTACCTGTCCCAAGACGCGCTGTGGCGGTGCCGACTTCT 538
Db 8589 SerThrSerAlaArgAlaArgSerAlaAlaSerAlaTrp-----8602
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QY 539 ACGTGAGCGCAAGTACGACCTGCGCCCTGCGCCAGATGCCCTGGTGGCGCCGTTTCTTCT 598
Db 8603 -----ThrThr-----ProAspArgThrThrAspAla 8611
QY 599 -----GGCGATCGATCTTCGACATCGACACCAATTCACATCGCGCCCGAGCGCC 646
Db 8612 TrpArgArgPheArgAspArgThrCysSerProThrThrProArgTrpArgArgCysAla 8631
QY 647 GGCCT--ACCTGGAGCAGAGCTGGAGCGG-----TGT 679
Db 8632 ArgProAspProTIPheArgSerArgSerAlaArgAlaThrTIPheThrThrSer 8651
QY 680 GGGAGCAGAACCCAGGTTGATCCCTACGTCCGCTGGC----- 721
Db 8652 GlySerSerValArgAlaArgThrProThrAlaValGlyGlyProSerSerSer 8671
QY 721 ----- 721
Db 8672 SerThrProThrArgProHisArgArgArgProGluArgCysAlaAlaGluArgGlnAla 8691
QY 722 -----TGCGCGCCCT----- 733
Db 8692 AspileGluArgGlnValArgGluSerPheGlyGlyLeuCysSerProProArgThrGly 8711
QY 734 -----ACTAGTGTGGATTGGCCGCTGCCAGCGTTGGCCACGCC--TGCAAGAGG 784
Db 8712 ArgAspileThrCysAlaTrpCysProTIPheArgCysAlaProArgAspThrArg 8731
QY 785 AGCGGTGG-----AGCGCGCGCCATGTTCGCGCCA 817
Db 8732 SerGlyTIPArgAlaArgArgArgAsnAlaGlySerProArgProAlaCysArgSer 8751
QY 818 CCTTCCTACACGCGAGTGGGAGGAGCCCGAGCGGATGGAGGTGATGGAGATCA 877
Db 8752 ArgCysSerThrArgArgThrTrpIysAlaProGly-----TIPArgSer 8766
QY 878 ACCCAAGGACACGGTGTGACCTGTAGCGCGCTGCAATGCCCTGAACCTGTGTGG 937
Db 8767 -----MetCysArgPro----- 8770
QY 938 TGC-----AGGGCGCGCCAGGTGG--TGTGGTGGACTGCACCCCGCGAGT 985
Db 8771 CysThrHisArgArgSerProValArgGlyArgCysArgCysThrArgSerProGlySer 8790
QY 986 CGGCGCTTCTGGAGCTGAAGAGGTGGCCATTACAGCAGCTGGAGTTTCAGGACGTGTGGC 1045
Db 8791 Arg-----CysSerArgSerThrThr 8797
QY 1046 AGCTGTTCGGCAGGGCGTGCACCGCGCATGTAGAGAGCTGTACGAGAAGAGCTGGCGC 1105
Db 8798 SerThrProAlaThrCysAlaThrSerGlyArgSerArgSerThrArgCysSerAlaAla 8817
QY 1106 CTTTCCTCTGCAACACGACGACACACTTCTGGTCCAAGCGCTCTGTACTTCCAGCAGC 1165
Db 8818 MetThrThrArgAlaSerAlaThrThrGlyGlyPro-----ThrTIPheCysThrThr 8835
QY 1166 GCCTGTACTACAGGGCGCATGGCAAGCTGTCTGGTGTCTGCAGTGCTGGCGCGTG 1225
Db 8836 SerTIPProSerArgAlaHisTIPSerProArgSerGlyAlaCysArgAla----- 8852
QY 1226 TGCTGGGAGTGGCAAGACCGTCAAGCGCTCGCAACCGCCGCCACAA----- 1273
Db 8853 -----SerMetCysArgProGlySerSerAlaProTIPArgProSerArgGlySerThr 8870
QY 1274 TGG-----AGGAGCAGCGCGTGTGGAGACGCAACA 1306
Db 8871 TrpSerArgThrArgCysArgAlaSerArgSerThrAlaSerSerGlyAlaAlaThr 8890
QY 1307 TGCTCATCCTTCGTGAAGAACGGGCCA-----AGCGGTGG--- 1345
Db 8891 GlySerSerThr-----ArgTIPThrProHisArgThrTIPArgCysArgArgTIPAla 8908

QY 1346 -----TGTGGCTGTTCGTCAGTTCTGTGAGCCTGTGCTCTTCAACAAGCGCG----- 1393
Db 8909 ThrArgCysGlyCysProCys-----AlaThrCysProThrThrAlaProArgAla 8925
QY 1394 -----TGCTGTGGTTCGCGCGCGGTGC 1417
Db 8926 ArgThrArgGlySerTIPArgSerGlyAlaAlaAlaCysAlaSerSerGlyAlaThr 8945
QY 1418 -----CGGCAAGCAGTACGCTGATCAAGCGGAGCGCATCCCCA---TTGAGAACT 1468
Db 8946 ArgProArgAlaSerSerAlaProThrTrpArgArgCysGlyThrProSerThrArgArg 8965
QY 1469 ACATCGCGCGCA-----CCATGGACGCGGTGGCGG 1498
Db 8966 CysGlyArgAlaArgArgTIPCysSerArgArgArgAsnArgTIPArgSerTIPGlu 8985
QY 1499 AGAATCGCACGTGGCAAGCAGAACTACTTCTACTACAACCTGCCTACCGSCAAAGTTCC 1558
Db 8986 ArgCysArg-----ProAlaSerGly 8992
QY 1559 TGCAGCAACTGCCACCTACCTGCGGAGGCGCTTCGCCACCTCAAGAGTGGCG 1618
Db 8993 CysCysAlaThrAla-----ArgTIPSerSerSerSerArgThrAla 9006
QY 1619 -----TGTGGACAACC--TGACCGTCTCCACCACTTCTTCATGGAGAGCTCAAG 1669
Db 9007 ThrCysTIPCysThrThrAlaAlaProThrAlaThrThrAlaSerTIPArgGlyPheArg 9026
QY 1670 CGCGCACCTACCAAGGTGATTCTGATGGACCACTGGCTGGCTGGATATGCCCGTGG 1729
Db 9027 SerCysProSerProSer-----ThrThr----- 9034
QY 1730 CCAACGAGCTGGCGAGTGGCTGCCAAGCAGGTTGGCGCGGGGCGCATCGTCACTGGC 1789
Db 9035 -----ThrArgSerAlaAlaAlaValSerIleProPro 9045
QY 1790 GCTCGGCT-----CCCTAGCGCGCTTACCGCGAGCTGATCCAGAAGCGGCGTTCG 1843
Db 9046 AlaProProCysProAlaLeuArgProArgProArgSerArgArgCysAla 9065
QY 1844 ACGTGC-----GCTGCATCGCGCGCGCACTCAGGGGTACATGACCGCGTCAACA 1894
Db 9066 GlyCysCysSerThrThrAlaThrAlaClyArgArgArgAenCysGlyThrAlaSerSer 9085
QY 1895 -----TGTCAGCTCCTTCTTACATGGCCCGCGCGA 1924
Db 9086 GlyHisLeuArgProProArgSerProGlyCys-----ProAlaSerTIPArgThrAla 9103
QY 1925 AGGCGCGCAAGAGCAACT 1945
Db 9104 GlyCysArgArgArgThrSer 9110
RESULT 10
US-10-084-846A-8
; Sequence 8, Application US/10084846A
; Publication No. US20040006026A1
; GENERAL INFORMATION:
; APPLICANT: WEITNAUER, GABRIELE
; APPLICANT: MUHLENWEG AGNES
; APPLICANT: TREFFZER, AXEL
; APPLICANT: BECHTHOLD, ANDREAS
; TITLE OF INVENTION: AVILAMYCIN DERIVATIVES
; FILE REFERENCE: 1974-005
; CURRENT APPLICATION NUMBER: US/10/084,846A
; PRIOR FILING DATE: 2003-02-25
; PRIOR APPLICATION NUMBER: PCT/EP01/09815
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: DE 101 09 166.4
; PRIOR FILING DATE: 2001-02-25
; NUMBER OF SEQ ID NOS: 120
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 8
; LENGTH: 19608

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; TYPE: PRT
; ORGANISM: Streptomyces viridochromogenes
; FEATURE:
; OTHER INFORMATION: Protein 3: amino acid sequence encoded by coding strand 1.
; OTHER INFORMATION: Start codon: atc, Start position: nucleotide 3.
US-10-084-846A-8

Alignment Scores:
Pred. No.:      5,05e-18      Length:      19608
Score:          436.00      Matches:      217
Percent Similarity: 35.0%      Conservative: 40
Best Local Similarity: 29.6%      Mismatches: 237
Query Match:      12.0%      Indels:      240
DB:               4         Gaps:        44

US-10-620-914-44 (1-1947) x US-10-084-846A-8 (1-19608)
QY 1939 CTTTCTTGGCGCCCTTCGGCGGGCCATGTAGAGGAGCTGTACATGTTGACGGGTCCA 1880
DB 10543 ProArgTrpArg-----CysProArg----- 10549
QY 1879 TGTAGCCCTGAGTGGCGGCGGATGACAGCGCAGCTCGAAGCCCGCCCTCTGTGATCAGCT 1820
DB 10350 -----ProArgArgProSerProThrAlaArgArgProProArgGlyGlySerAla 10567
QY 1819 CGGCGTAGGCGGGCTGAGGAGGCGGAGCCAGATCACCATGCCCGCCGCGCAACCT 1760
DB 10568 AlaArgArgPro-----ArgArgAlaLysValProAlaArgArgProAlaValSer 10585
QY 1759 GCTTGGCCAGCAGCTCGGCCAGCTGCTGGCGACGGGCATATCAGCCAGGTCACAGTGGT 1700
DB 10586 ProProGlyGlySerGlyGlyArg-----ThrAlaProGlyAlaAlaProProArg 10603
QY 1699 CCATCAGAATCACCCTTGCTGAGTGGCGCTTTGAGCTCTCCATGAAAGATTGGTGG 1640
DB 10604 ProSerArg---ProTrpProGln----- 10610
QY 1639 AGACGTCAGTTGTCACACAGCCACTCTTGAGGTGGCGAAGCCGCCCTCGC---GCA 1593
DB 10611 GlyArgThrGlySer-----GlyTrpArgArgArgArgGly 10624
QY 1582 GGTAGGTGGGCGAGTTGTCGCGCAGGAACCTTGCCGGTGAGGCAGTTGTAGTAGAAGTAGT 1523
DB 10625 GlyArgArgSerAlaCysArgSerGly-----ArgGlyThr 10636
QY 1522 TCTGCTTGGCAGCTGCGAGTTCTCCGCCACGCCGTCATGGTGGCGCGCATGTAGTTCT 1463
DB 10637 Ala-----AlaGluSerProProArg-----CysArgSerCysSerSer 10649
QY 1462 CAATGGGATGCGCTCCGCTTGATCAGCGGTACT-----GCT 1424
DB 10650 ---TrpArgCysArgGlyAlaProAlaGlyArgSerThrGlyAlaProAlaGlySer 10668
QY 1423 TGCCCGGACGCGCGCGCGGCAACACACAGCAGCGGCTTGTGAAGAGCAGCAGGCTCACGA 1364
DB 10669 CysAlaAlaProGlyArgArgProAlaAlaLeuPro-----AlaPro----- 10682
QY 1363 ACTTGACGAACAGCCACACACAGCGGCTTGGCGCCGCTTCTTCCAGAAAGTGATGATGT 1304
DB 10683 -----ProProValProAlaAlaProAlaPro----- 10691
QY 1303 TGCTGTCCACAGAGCGGCTGCTCTCCATGTGGGCGGCTTGGCGAGGCGCT----- 1250
DB 10692 -----ProProArgProAlaAlaProPro-----ArgArgTrpArgAlaAlaPro 10707
QY 1249 -----TGACGGTCTTGCCAGTCCAGCA---CCACGG----- 1220
DB 10708 ValArgArgArgArgArgCysProArgProSerCysProArgArgCysThrArgValCys 10727
QY 1219 CCAGGCATGTGAGCAGCACCAGCAGCTTGGCCATCGCCCTGTGTAGTACAGGCGGTGCT 1160
DB 10728 ProGly---SerAlaProAlaAlaThrGlyPro---ArgProGlyArgArgCysArgAla 10745
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QY 1159 GGAAGTACCAGAGCGCTTGGACCAGAAAGTTGTGGCTTTCGACAGGAAGGCGCCA 1100
DB 10746 ArgSer-----AlaTrpAlaAlaAlaAlaArgPro 10756
QY 1099 GCTTCTTCTCGTACAGCTCCTCAATGCGGGGTGCAGCCCTCCGCAACAGCTGCCACA 1040
DB 10757 Ala-----AlaAlaProProArgProValArgGly 10766
QY 1039 GTCCTCAAACTCCAGCTGCTGAATGGCCACCTTCTTCAGCTCCAGAAAGCCGCACTCGC 980
DB 10767 ProProArgThrGlySerGlyArgGlyProThrArgArgArgThrSerArgSerThr 10786
QY 979 CGGGTTGTCAGTCCACGACACACACCTGGCGGCGCCCTGCACACAGAGGTTCAAGGCAT 920
DB 10787 AlaGly-----ProProArgProGlyArg-----AlaProAlaArgSerProArg 10801
QY 919 TGCAGCCGCGCTAGTACAGGCTCAGCACCCGTGT---CCTTGGGTTGATCTCCA---TCA 866
DB 10802 CysArgThrArgAlaThrHisArgSerAlaArgProGlyAlaAlaArgProValArg 10821
QY 865 CTTCCATATCCGGCTCGGGTCTCCACGACTCGGTGTACAGAGGTGGCGGGAACA 806
DB 10822 ProArgArgProCysArgAlaProProGlyArgAlaAlaSerGlyArgArgSerPro 10841
QY 805 TGGCGCGCGCTCCACGCGCTCTCGTGCAGGCGTGGCCAACTGGGCGAGCGGCCAA 746
DB 10842 ArgCysHisSerCysAlaAlaProArgArgSerThrSerArgSerArgAlaGlyArg 10861
QY 745 TCCACACGTAGTAGGGGCGCGCAGCCACGCGCAGTAGGGATCCAAACCTTGGGTGTTCT 686
DB 10862 ArgArgArgSerArgAlaThrAlaSerAlaAlaArgThrGlyAlaAlaAlaAlaAla 10881
QY 685 GCTCCACACGCGCTCCAGCTTCTGCTCAGGTAGGCGCGCGCTCGGGCGCGATGTCAA 626
DB 10882 AspArgThrAlaAlaValCysThrTrpProAlaHisArgThrProAlaGlyArgPhePro 10901
QY 625 TGTGTGCGATGTCGAAGATCGATCCGAGAAAGCGCGCAGCAGG----- 578
DB 10902 SerCysProAlaArgAlaProGlyProAlaSerGlyArgSerArgArgProArgVal 10921
QY 577 -----GCATCTGGCGCA 566
DB 10922 ProAlaThrAlaGlyThrProProGlySerArgValProArgAlaAlaProArgPro 10941
QY 565 GGGCAGGTGCTACTTCCCG-----TCAGTAGA-----AGTCGCGCAACGC 524
DB 10942 GlyAlaProCysThrCysAsnValProProSerSerArgArgThrSerSerSerGluArg 10961
QY 523 CCACCA-----GGCCGCTCTTGGGACAGGT 500
DB 10962 LeuProAspLeuProPheAspValCysLeuAlaLeuGlyGlyAlaAlaLeuArgAlaPro 10981
QY 499 ACGAGCAAGCTGTGTCATGACGTTGTGGAAACGGTGAATCATCGTAGCGCAGTAGGAGA 440
DB 10982 AlaValArgProGlyArg-----ArgThrArg 10990
QY 439 AGGTGATGAGCGCTCGCGTGC-----CCTCAGGGGCGCAATTTGGCAAG 395
DB 10991 ArgTrpSerAlaAlaAsnCysArgTrpArgSerGlyProAsnArgGlyArgAlaGlyArg 11010
QY 394 CGTCGGCTCCA---CGACCTGGACATTTCTCCAGCCCTTGGCCTTCGCTC----- 347
DB 11011 ArgAlaProProArgArgProGly-----ProGlyProGluProArgValArg 11026
QY 346 -----TCTTCTGCCCACTTCGCACACGAGTGGCACAGT----- 311
DB 11027 SerArgAlaProSerProProArgArgArgGlyAlaGlyAlaAlaProGluProPro 11046
QY 310 -----CGACCAGTAGATGACT----- 293
DB 11047 ProGlyIleArgCysAlaValArgArgProGlyArgCysSerAspCysArgProCys 11066
QY 292 -----TGAACCTTCGCCAGGT 278
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Db 11067 AlaGlyArgArgGlyHisGlyAlaMetaLaProProArgProGlyThrAlaProGly 11086
QY 277 CGATGTAATCAGCCATCATATCGACATTCTCCAGTGCACACCCAGGTCAACCCAGA 218
Db 11087 ArgAlaArgArgArgTIPAlaArg-----ProGlyArgProArg 11099
QY 217 TGAGTTCCAGCGCTCGG-----CCAGCGGGCAGCAAGAGCAGCGGCTGGGCCCCGT 164
Db 11100 ThrArgArgArgAlaAlaProValProArgGlyAlaAlaGlyProValProGlyProSer 11119
QY 163 AGAGCTCTCCA-----GGCGAGCAGCGTGAT---CATCGCCCT----- 128
Db 11120 ProAlaSerProSerCysAlaArgGlyArgGlyArgAspAlaHisArgProArgArgGly 11139
QY 127 ---TCTTGTCTGCGCAACCATATATGCGCGCAGCAACCGTCAGGT 89
Db 11140 SerSerSerArgArgSerAlaGlyProArgArgSerGly 11153

RESULT 11
US-10-084-846A-4
; Sequence 4, Application US/10084846A
; Publication No. US20040006026A1
; GENERAL INFORMATION:
; APPLICANT: WEITNAUER, GABRIELE
; APPLICANT: MUHLWENEG, AGNES
; APPLICANT: TREFFZER, AXEL
; APPLICANT: BECHTHOLD, ANDREAS
; TITLE OF INVENTION: AVILAMYCIN DERIVATIVES
; FILE REFERENCE: 1974-005
; CURRENT APPLICATION NUMBER: US/10/084,846A
; CURRENT FILING DATE: 2003-02-25
; PRIOR APPLICATION NUMBER: PCT/EP01/09815
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: DE 101 09 166.4
; PRIOR FILING DATE: 2001-02-25
; NUMBER OF SEQ ID NOS: 120
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 4
; LENGTH: 19725
; TYPE: PRT
; ORGANISM: Streptomyces viridochromogenes
; FEATURE:
; OTHER INFORMATION: Protein 2: amino acid sequence encoded by coding strand 1.
; OTHER INFORMATION: Start codon: gat, Start position: nucleotide 2.
US-10-084-846A-4

Alignment Scores:
Pred. No.: 2,77e-17 Length: 19725
Score: 424.00 Matches: 222
Percent Similarity: 33.2% Conservative: 41
Best Local Similarity: 28.0% Mismatches: 251
Query Match: 11.7% Indels: 278
DB: 4 Gaps: 49

US-10-620-914-44 (1-1947) x US-10-084-846A-4 (1-19725)
QY 1939 CTTCTTGGCGCCCTTCCGGCGGCGCATGTAGAGGAGCTGTACATGTTGACGGGTCCA 1880
Db 17234 ProSer---ArgProTyrGlyArgProTrpAsnArgSerMetSerAsnTrpProGly--- 17251
QY 1879 TGTAGCCCTGATGGCGCGC-----GGATGCGACGCGACGTCGTAAGCCCGCT 1832
Db 17252 -----AlaSerTrpArgSerSerArgTrpProGlyCys-----ArgThrSerProArg 17267
QY 1831 TCTGATCAGCT-----CGGGGTAGGGCGGCTGAGGAGCGGAGC----- 1790
Db 17268 AlaGlyCysAlaTrpGlyArgTrpArgArgAlaGlySerGlyArgSerAlaArgCysSer 17287
QY 1789 -----GCCAGATGACGATGCGCGCGCGCAACCTGCTTGGCCAGGACCTCGGCCA--- 1739
Db 17288 ThrProAlaArgThrGlyCys-----AlaSerSerAlaGlySerGlySerArgProPro 17305

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QY 1738 ---GCTCGTTGG-----CCACGGGCATAT---CCAGCCAGTCCA--- 1706
Db 17306 ThrArgArgTrpProProProSerGlySerProArgLeuTyrGlyThrAlaSerProTyr 17325
QY 1705 -----CGTGGTCCATCAGAAACACT---TGG-----TGTAGGTGC 1673
Db 17326 ThrSerThrTrpThrGlyProSerProGlyProProHisTrpSerSerArgCysThrCys 17345
QY 1672 CGCTTTGAGCTCTCCATGAAGAAGTTGGTGGAGACGGTCAGGTTGTCCACCCAGCCAC 1613
Db 17346 -----TrpTrpArgArgAla-----ProArgHis 17353
QY 1612 TCTTGGGGTGGCAGGCGG-----;-----CCTCGCGCA 1583
Db 17354 AlaGlyProSerArgArgAlaGlyArgArgSerSerAlaArgCysTrpProArgArg 17373
QY 1582 GGTAGGTGGGCGAGTTGTGCGCGCAGGAACCTTGCCTGAGGAGTGTAGTAGA----- 1529
Db 17374 GlyArg-----ArgGlnAlaGlyCys-----AlaCysCysSerArgGlyGly 17387
QY 1528 -----AGT-----AGT 1526
Db 17388 ProHisGlyAspGlyArgTIPArgProTrpArgArgSerAlaHisProSerArgProThr 17407
QY 1525 AGTTCTGCTTGGCGACGTGCGAGTTCCTCCGCCAGCCGTCATGGTGCAGGATGTAGT 1466
Db 17408 ThrThrValCysHisArgCysSerProArgProArgSerThrCysCysAlaAlaArgAla 17427
QY 1465 TCTCAATGG-----GGATGCGCTCGCGCTTGATCAGCGCGTACTGCT 1424
Db 17428 ProArgTrpProProTrpSerThrSerCysAlaProPro-----SerThrThrAla 17445
QY 1423 TGCCCGCGCAGCCCGCGCCAAACACAGCAGCGGCTTGTGAAGAGCACCA----- 1373
Db 17446 CysSerProSerSerArg-----AlaAlaProProThrProArgArgProArgGlySer 17463
QY 1372 -----GGTCACGAACCTTGACGAACAGCACCCACCGG 1340
Db 17464 CysArgThrArgTrpProSerGlySerGlyProArgArgSerThrThrArgThrAlaGly 17483
QY 1339 GCTTGGGCGCGTCTTCACGAAGTGGATGACATGTTGCTGCCACAGACGGCGCTGCT 1280
Db 17484 SerHisCysAlaAlaThrArgProSer---AlaProAlaSerProSerProSerAlaGly 17502
QY 1279 CCTCCATTGTGGGCGGTGGCGAGGCGCTTGACGGCTCTGCCAGCTCCAGCACCCACGG 1220
Db 17503 ArgSerSerAlaThrArgTrpGlySerAlaArgArgSerArgProSerProHisSerArg 17522
QY 1219 -----CCAGGC 1214
Db 17523 ThrProProArgGlyArgAlaThrSerTrpTrpSerValArgProAlaCysSerThrGly 17542
QY 1213 ACTGACGACCCAGCACAGCTTGCCCATGCGCCCTGGTAGTACAGGCGGTGCTGGAAGT 1154
Db 17543 ProGlyArgProArgSerAlaValCysCysAlaHisArgCysThrAlaProThrGlyArg 17562
QY 1153 ACCAGAGCGCGTTCGACAGCAAGTGTGGTGGTTGCGACAGGAAGCGCCAGCTTCT 1094
Db 17563 ThrArgSer-----ProThrGlyArgGlyGlyAlaAla 17573
QY 1093 TCTCGTACAGCTCTCAATGCGGGGTGACGCCCTGCGCAACAGCTGCC----- 1043
Db 17574 SerArgSerProProSerThrArgCysGlyAlaSerArgArgProGlyAlaAlaArgTrp 17593
QY 1042 -----ACAGTCTCTCAACT-----CCAGTGTGTAATGGCCA 1010
Db 17594 AlaCysSerSerTrpThrArgProThrThrArgIleProGlyProAlaAlaProTrpPro 17613
QY 1009 CTTTCTTCAGCTCCAGGAAGCGCCGACCTGCGGGGTTCAGTCCACCGACACCCAGTGGC 950
Db 17614 SerProSerGly-----ArgSerThrAlaThrAlaCysCysSerProValArgProTrp 17631
QY 949 CGGCCCCCTGCACCCAGCAGGTTTCAGGGCATTTGACGGCCCGCTAGTCAGGGTTCAGCACCG 890

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Db 17632 ArgThrAlaSerArgSerSerAlaAlaTrpCys-----GlySerSerSer 17646
Qy 889 TGTCTTGGGGTTGATCTCCATCACCTCCATATCGGGCTCGGGTCTCTCCACAGCTGCG 830
Db 17647 ProSerTrp-----ArgArgProSerThrSer--- 17655
Qy 829 TGTACAGGAAGTGGCGGGAACATGGCGCGCGCTCCACGGCTCTCTCGTCGAGGGCGT 770
Db 17656 ---ThrThrAlaTrp-----ArgAlaProArg----- 17663
Qy 769 GGCCAAACGCTGGCAGCGCGCAATCCACAGCTAGTAGGGGCGC-----GCAGCC 719
Db 17664 -----ArgSerAlaArgArgSerHisArgSerIleCysAlaAla 17676
Qy 718 ACGCACGTAGGGATCGAACCCCTGGGGTTCGTCTGCCACACGCGCTCCAGCTTCGTCT 659
Db 17677 ThrSerArgThrSerSerProAsnSerArgArgSerSerThrArgThrSerGlyArgSer 17696
Qy 658 CCAGTAGGCGCGGCTCGGGCGCGATGTCATGTTGTCGATGTCGAGATCGATCGCC 599
Db 17697 ProAlaArgArg-----Thr 17701
Qy 598 AGAAGAAACGCGGACCCAGGGCATCTGGCGCAGGGCAGGTCTGTAATCTTCCGCTCAGT 539
Db 17702 ArgArgProThrAlaArgProCysAlaProAlaThrSerTrpArg---CysAlaGlyArg 17720
Qy 538 AGAAGTGGCAACCCCAACAGGCGCTCTGGGACAGTACGACGACGAGCTGTGATGA 479
Db 17721 ArgThrArgValArgSerGlyProArgArgCysThrGlyCysAlaArg----- 17736
Qy 478 CGTTGTGGAACGGTGGATCATCTGACGAGTAGGAGAGGTGATGACGCTCGGGTGC 419
Db 17736 ----- 17736
Qy 418 CCTCAGGGGGCAAAATGGCAAGCGTCTGGGCTCCAGCCTGGACATTTCTCCAGCCCT 359
Db 17737 -----SerLeuArgArgProProAlaThrGlyArgSer----- 17747
Qy 358 TGGGCTTCGCTCTTCT-----TGGCCA-----CCTCGACACGCG 323
Db 17748 TrpCysSerProArgSerGlyThrTrpTrpGlnTrpTyrAlaArgArgSerArgThrArg 17767
Qy 322 AGTGGCACAGTCCACACAGT---AGATGGACTTCACTTCGCCAGGTTCGATGTAATCAG 266
Db 17768 ProGlyGlnGlyArgGlyGlnAlaArgArgThrSerArgGlyProLysArg---GlyGlu 17786
Qy 265 CCATCATATCGACATTTCTCCAGTGCACCCAGCCAGGTCAACCCAGATGAGGTTTCGAGC 206
Db 17787 ProGlnArgMetArgGlyAlaArg---ArgTrpLysGlyGlnProArgArgThrArgArg 17805
Qy 205 GCTCG-----CCAGGGGGCAGCAAGGCAG-----CGG 176
Db 17806 AlaArgArgSerProProTrpGlyThrHisArgArgArgSerGlyArgGlyArg 17825
Qy 175 CTGGGGCCCTAGAGCTCTCCAGGCGAGCGGTGATCATCGCCCTTCTTGTGTCGCA 116
Db 17826 AlaGlyCysArgAspArgGlyProGlyValCysSerGlyArgSerArgAlaAlaCysArg 17845
Qy 115 -----ACCACATATGCGCAGAACCGTCAAGGTCACTTCATGTC 77
Db 17846 ProProAlaAspSerSerSerSerThrThrSerProProArgProValThrProTyrCys 17865
Qy 76 TGCTGAGCTTGAGCTTCTCCAGGGAGAGTCTCTTCTGCTGATG----- 32
Db 17866 -----SerArgArgSerArgGlnAlaGluTrpAlaSerThrCysArgProPro 17881
Qy 31 -----TCGACAGGCGCGCTCAGCACCGCCGCCA 2
Db 17882 ProTrpSerSerAlaSerArgSerSerSerArgPro 17893
RESULT 12
us-10-084-846A-4
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; Sequence 4, Application US/10084846A
; Publication No. US20040006026A1
; GENERAL INFORMATION:
; APPLICANT: WEITNAUER, GABRIELE
; APPLICANT: MUHLENWEG, AGNES
; APPLICANT: TREFFZER, AXEL
; APPLICANT: BECHTHOLD, ANDREAS
; TITLE OF INVENTION: AVILAMYCIN DERIVATIVES
; FILE REFERENCE: 1974-005
; CURRENT APPLICATION NUMBER: US/10/084, 846A
; CURRENT FILING DATE: 2003-02-25
; PRIOR APPLICATION NUMBER: PCT/EP01/09815
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: DE 101 09 166.4
; PRIOR FILING DATE: 2001-02-25
; NUMBER OF SEQ ID NOS: 120
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 4
; LENGTH: 19725
; TYPE: PRT
; ORGANISM: Streptomyces viridochromogenes
; FEATURE:
; OTHER INFORMATION: Protein 2: amino acid sequence encoded by coding strand 1.
; OTHER INFORMATION: Start codon: gat, Start position: nucleotide 2.
US-10-084-846A-4
Alignment Scores:
Pred. No.: 3,07e-16 Length: 19725
Score: 407.00 Matches: 236
Percent Similarity: 34.8% Conservative: 48
Best Local Similarity: 29.0% Mismatches: 237
Query Match: 11.2% Indels: 294
DB: 4 Gaps: 53
US-10-620-914-44 (1-1947) x US-10-084-846A-4 (1-19725)
Qy 23 GGCCTGGGAGCTACACCAAGAAGAACTTCTCCCTGG-----AGAAGCTCAAGC 70
Db 17261 GlyCysArgThrSerProArgAlaGlyCysAlaTrpGlyArgTrpArgArgAlaGlySer 17280
Qy 71 TCACAGCATGATGAGGATGACCTGACCGTTCGCGCATATGTGTTCGGCAGCAAGAGG 130
Db 17281 GlyArgSer-----AlaArgCysSerThrProAlaArg--- 17291
Qy 131 CGCATGATCAGCTGCTCGCTGGAGAGCTTCTACGGSCCCAGCGCTGCTTGTCTG 190
Db 17292 -----ThrGlyCysAlaSerSerAlaGlySerGlySerArgPro--- 17304
Qy 191 CCCGCC-----TGGCCGAGCGCTCGAACCTCATCTGGGTTGACCTGGGTGGTGGCACTG 244
Db 17305 ProThrArgArgTrpProProSerGlySerProArgLeu-----Tyr 17319
Qy 245 GGGAGAATGTCGATATGATGCTGATTACATCGACCTGGCGAAGTTCAAGTCCATCTAGC 304
Db 17320 GlyThrAlaSer-----ProTyrThrSerThrTrpThrGlyProSerProGlyPro 17336
Qy 305 -----TGGTTCGACCTGCGCTGCTGCGAGGTGGCCCAAGAGA----- 346
Db 17337 ProHisTrpSer-----SerArgCysThrCysTrpTrpArgArgAlaProArgHis 17353
Qy 347 -----AGCGAAGG-----CCAAGGCT 364
Db 17354 AlaGlyProSerArgArgAlaGlyArgArgSerSerAlaArgCysTrpProArgArg 17373
Qy 365 GGAGA-----ATGTCAGGTCTG----- 382
Db 17374 GlyArgArgGlnAlaGlyCysAlaCysCysSerArgGlyGlyProHisGlyAspGlyArg 17393
Qy 383 TGGAGGCGGACGCTGGCCAAATTTGGCCCGCTGAGGCGCCAGC-----CGAGCG 430
Db 17394 TrpArgProTrpArgArgSerAlaHisProSerArgProThrThrValCysHisArg 17413
Qy 431 TCATCACCTTCTCTACTCGCTCGATGATTCCACCGTTCACACCGTTCATCGACCCAGG 490
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Db 17414 CysSerProArgPro-----ArgSerThrCysCysAlaAlaArg 17426
QY 491 CTTGCTCGTACCTGCCAAGACGGCTGGTGGGGTTCGACCTTCTACGTGAGCGGCA 550
Db 17427 AlaProArgTppProTppSerThrSerSerCysAlaProProSerThrThrAlaCys 17446
QY 551 AGTACGACTGC-----CCCTGGCGCAGATGCCCTCGT 583
Db 17447 SerProSerSerArgAlaAlaProProThrProArgArgProArgGlySerCysArgThr 17466
QY 584 CGCGCGGTTCT---TCTGGCGATCGATCTCGACATCGACACATTCGACATCG--- 634
Db 17467 ArgTppProSerGlySerGlyProArgArgSerThrThrArgThrAlaGlySerHisCys 17486
QY 635 -----GCCCGGAGCGCGCGCTACCTCGGAGC 661
Db 17487 AlaAlaThrArgProSerAlaProAlaSerProSerProSerAlaGlyArgSerSerAla 17506
QY 662 AGAAGCTGG---AGCGGTGGGAGCAGA---ACACCCAGGGTTTCATCCCTACGTGC 715
Db 17507 ThrArgTppGlySerAlaArgArgSerArgProSerProHisSerArgThrProPro--- 17525
QY 716 CGTGGCTGGCGCCCTACTACGTGTGGATTGGCGGCTGCCACGCTGGCCACGCC 775
Db 17526 ArgGlyArgAla----- 17529
QY 776 TGCAGGAGCGCGCTGGAGCGCGCCCA---TGTTC---CGCCCACT 820
Db 17530 -----ThrSerTppSerValArgProAlaCysSerThrGlyProGlyArgProArg 17547
QY 821 TCC-----TGTAACGACGTCTGGAGAGACCCGACCGCGGATA 859
Db 17548 SerAlaValCysCysAlaHisArgCysThrAlaProThrGlyArgThrArgSerProThr 17567
QY 860 TGGAGGTATGG-----AGATCAACCCNAGCACACGTGTGACCTGACTAGCG 910
Db 17568 GlyArgGlyAlaAlaSerArgSerProProSerThrArgCys-----Gly 17583
QY 911 CGCGTGAATGCCCTGAACCTGCTGGTGCAGGGGGCGCGCAGGTGGTGT-----CGG 964
Db 17584 AlaSerArgArgPro-----GlyAlaAlaArgTppAlaCysSerSer 17597
QY 965 TGGACTGCAACCCCGCAGTGGCGCTTCTGGAGCTGAAGAAGTGGCCATTGACGACG 1024
Db 17598 TrpThr---ArgProThrThrArgileProGlyProAlaAlaProTppProSerProSer 17616
QY 1025 TGGAGTTGAGGACGTGGCAGCTGTTCGGCGAGGGCGTGACCCCGCATTTGAGGAGC 1084
Db 17617 -----GlyArgSerThrAlaThrAlaCysCysSerProVal----- 17628
QY 1085 TGTACGAGAAGCTGGCGCTTCTGTGCAAAACAGCACCACTTCTGTGTCACAGC 1144
Db 17629 -----ArgProTppArgThrAlaSerArgSerSerAlaAlaTppCysGlySerSer 17645
QY 1145 GCC-----TCTGGTACTTCCAGCAGCGCC-----TGTACTACCGAGGCGC 1183
Db 17646 SerProSerTppArgArgProSerThrSerThrAlaTppArgAlaProArgArgSer 17665
QY 1184 GCATGGGCAAGCTGTGGGTGTCGACGTGCTGGCGCTGGTGTGGGACTGGGCAGA 1243
Db 17666 AlaArgArgSerHisArgSerIleCysAlaAla-----ThrSerArg 17679
QY 1244 CGCTCAAGC-----GCCTCGCAAGCGCCCAATGAGGAGGAGCGGCC--- 1288
Db 17680 ThrSerSerProAsnSerArgArgSerSerThrArgThrSerGlyArgSerProAlaArg 17699
QY 1289 -----GTCTGTGGGACAGCAACA-----TGCTCATCC 1315
Db 17700 ArgThrArgArgProThrAlaArgProCysAlaProAlaThrSerTppArgCysAlaGly 17719
QY 1316 -----ACTTCGTGAAGACGGGCCCAAGCGCTGGTGTGCTGTTCGTCAAGT----- 1363
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Db 17720 ArgArgThrArgValArgSerGlyProArgArgCysThrGlyCysAlaArgSerLeuArg 17739
QY 1364 -----TCGTGAGCCTGGTGC----- 1378
Db 17740 ArgProProArgThrGlyArgSerTppCysSerProArgSerGlyThrTppGlnTpp 17759
QY 1379 -----TCTTCAACAGCGCGTGTGGTTCGGCGCGCGTGCCTGGCGGCAAGC 1426
Db 17760 TyrAlaArgArgSerArgThrArgProGlyGlnGlyArgGlnAlaArgArgThrSer 17779
QY 1427 -----AGTAGCGCTCATCAAGCGCGAGCGGACGCCATCCCA 1459
Db 17780 ArgGlyProLysArgGlyGluProGlnArgMetArgGlyAlaArgArgTppLysGln 17799
QY 1460 TTGAGAACTACATCGCGCGCA-----CCATGGACCGCGTGGCGGAGAACT 1504
Db 17800 ProArgThrArgArgAlaArgArgArgSerProTppGlyThrHisArgArg 17819
QY 1505 CGCAGC-----TGCCCAAGCAGA 1522
Db 17820 ArgSerGlyArgGlyArgAlaGlyCysArgAspArgGlyProGlyValCysSerGlyArg 17839
QY 1523 ACTACTTCTACTACAACTGCCTCACCGGCAAGTTCCTCGCGACAACTGCCCCACTACC 1582
Db 17840 SerArgAlaAlaCysArgProProAlaAspSerSerSerThrThrSerProProArg 17859
QY 1583 -----TGGCGAGCGCGCTTTCGCCACCTCAAGAGTGGCGTGGTGG--- 1624
Db 17860 ProValThrProTppCysSerArgArg-----SerArgGlnAlaGluTppAla 17875
QY 1625 ---ACAACCTGACGTCTCCACCACTTCTTCATGGAGGAGCTCA----- 1666
Db 17876 SerThrCysArgProProTppSerSerAlaSerArgSerSerArgProSerAsn 17895
QY 1667 ---AAGCGCGCACCTACACCAAGGTGATTCTGATGGACCACTGGACTGGCTGG--- 1717
Db 17896 ThrArgArgSerProValPro-----ThrAlaTppAlaArg 17907
QY 1718 -----ATATGCCCTGGCCCAAGAGCTGGCGGAGTGGCTGGCGCA 1756
Db 17908 SerAlaArgSerAlaCysThrAlaCysSerAlaArgLysGlyTppThrAsnAlaTppCys 17927
QY 1757 AGCAGTTGGCGCGGGGCGCATCGTCATCTGGCGCTCGCTCCCTCCCTAGCGCGCTAG 1816
Db 17928 GlyCysTppArgThrSerProAlaCysSerThrLeuThrProAlaAlaAlaArg----- 17945
QY 1817 CCGAGCTGATCCAGAGCGGCGCTTCGACGTGCGCTGCATCCGCGCGCCACTCAGGGCT 1876
Db 17946 ---SerProSerArgHisArg----- 17951
QY 1877 ACATGGACCGCGTCAACATGTACAGCTCTTCTACATGGCGCGCC 1921
Db 17952 -----ThrProSerThr---SerArgThrSerProTppProAla 17963
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RESULT 13

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US-10-084-846A-3
; Sequence 3, Application US/10084846A
; Publication No. US20040006026A1
; GENERAL INFORMATION:
; APPLICANT: WEITNAUER, GABRIELE
; APPLICANT: MUHLENWEG, AGNES
; APPLICANT: TREFFZER, AXEL
; APPLICANT: BECHTHOLD, ANDREAS
; TITLE OF INVENTION: AVILAMYCIN DERIVATIVES
; FILE REFERENCE: 1974-005
; CURRENT APPLICATION NUMBER: US/10/084,846A
; CURRENT FILING DATE: 2003-02-25
; PRIOR APPLICATION NUMBER: PCT/EP01/09815
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: DE 101 09 166.4
; PRIOR FILING DATE: 2001-02-25
; NUMBER OF SEQ ID NOS: 120
; SOFTWARE: Patent in Ver. 3.2
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; SEQ ID NO 3
; LENGTH: 19695
; TYPE: PRT
; ORGANISM: Streptomyces viridochromogenes
; FEATURE:
; OTHER INFORMATION: Protein 1: amino acid sequence encoded by coding strand 1.
; OTHER INFORMATION: Start codon: gga, Start position: nucleotide 1.
US-10-084-846A-3

Alignment Scores:
Pred. No.:      8,56e-15      Length:      19695
Score:          383.50      Matches:      218
Percent Similarity: 34.2%      Conservative: 57
Best Local Similarity: 27.1%      Mismatches: 268
Query Match:      10.6%      Indels:      260
DB:               4         Gaps:        48

US-10-620-914-44 (1-1947) x US-10-084-846A-3 (1-19695)
QY  1945 AGTTGTCTCT---TCTTGGCGC-----CCTTCGGCGGGCCATGTAGA 1907
DB  4930 SerCysValIleGlyTrpArgHisArgAlaLaProProAlaCysLeuProCysAla 4949
QY  1906 -----AGGAGCTGTACATGTTGACGCGGTCCATGT-----AGCCCTCAGTGG 1865
DB  4950 CysCysArgCysCysArgCysTrpProArgProCysCysGlyThrAlaProArgAla 4969
QY  1864 CGCGCGGATCAGCGCAGTCGAGAGCCCGCTTCTGGATCAGCTCGGCGTAGGCGGGC 1805
DB  4970 Arg-----ThrThrArgArgAspProAlaProGlyValProArgArg-----Gly 4984
QY  1804 TGAGGAGCGGAGCGGCAGATGACGATCGCGCGCGCGCAACCTGCTTGGCCAGGCAC 1745
DB  4985 MetArgArgMetSerArgArgGlyGlyCysCysSerProSerProTrpTrp----- 5001
QY  1744 CGGCAGCTCGTTGGCCACGCGGCATATCCAGCCAGTCCACGTCGTCCTCAGAA----- 1691
DB  5002 -----TrpPro-----SerArgGlyProAlaGluArgTrp 5011
QY  1690 -----TCACCTTGTGTAGTGGCGGCTTTGAGCTCCTCCATGAGAAAGTTGTGGAGA 1637
DB  5012 SerAlaGlyThrTrpAlaSer-----HisAlaTrpTrpAla 5023
QY  1636 CGGTACAGTTGTCCACACAGCCACTCTTGAGGTGGCGAAGCGCCCTCGCGCAGGTAGG 1577
DB  5024 ArgSer-----ProGlySer 5028
QY  1576 TGGGCGAGTTGTGCGCAGGAACCTTGGCGGTGAGGAGTTGTAGTAGAAGTAGT----- 1523
DB  5029 PheSerAlaLeuArg-----CysSerAlaSerSerLeuPro 5040
QY  1522 TCTGCTTCGGCAGTGGCGAGTTCTCCGCGCAGCGCGTCCA----- 1484
DB  5041 GlySerThrThrProSerSerProProProSerThrProThrSerIleSerSerProArg 5060
QY  1483 -----TGGTGGCGGATGATGTTCAATGGGATGCCGCTCGCCTTGATCAGCGGT 1430
DB  5061 SerGlyTrpArgCysSerCysSerSerAlaTrpSerSerValThrProThrMetIysAla 5080
QY  1429 ACTGCTTCGCGCAGCGCGCGCGCAACACACAGCAGCGCGCTTGTGTAAGACACCGAGC 1370
DB  5081 ArgAlaAlaProGlyProProTrpGluSerSerAlaSerAlaCys---ArgSerProSer 5099
QY  1369 TCAGAACTTGACGAAACA---GCCACACAGCGGCTTGGGCGCGCTTCTTCAAGAGTGA 1313
DB  5100 AlaValLeuTrpAspThrArgCysThrProAlaThrProArgThrAlaSerAlaSer--- 5118
QY  1312 TGACATGTTGCTGTCCACAGACGGCGCTGCTCT-----CCATTGGGCG 1265
DB  5119 -----CysArgSerProSerSerTrpAlaSerProAlaProProSerProCysTrpArg 5136
QY  1264 CGTTGGCGAGGCGCTTGACGGTCTTGCCAGTCCCGACGACCGCCAGGCACCTGCAGCA 1205
```



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QY 343 TCT-----TGCCCA----- 335
Db 5488 ThrSerProLeuArgLysTrpProCysGlyArgArgSerArgArgGlyGlyAlaAlaAsp 5507
QY 334 -----CCTCGCAGCAGGTGGCACA--- 314
Db 5508 ArgArgArgAsnSerIleCysCysMetArgAlaProGlyThrArgAlaArgThrAla 5527
QY 313 GGTCCACCACGTAGA-----TGGACTTGAAC-----TCGCCA----- 281
Db 5528 GlyArgProArgHisThrCysSerGlyThrTrpTrpAlaGlyThrCysSerProTrparg 5547
QY 280 -----GGTCATGTAATCAGCCATCATCATCGACATCT 248
Db 5548 SerGlyArgAlaAlaThrAlaCysSerAlaArgTrpAsnSerProSer--AlaThrCysA 5567
QY 247 CCCAGTG-----CCACCACCCAGGTCAACCCAGATGAGTTGG 209
Db 5567 rgProIleArgThrAlaProAlaArgSerSerProProThrThrThrGluArgArg-Ser 5586
QY 208 AGCGTCGGCCAGGCGG-----CAGCAAGGCGAGCGGCTGGG 170
Db 5587 ThrGly-----GlyGlyTrpAlaProAlaSerSerAlaAlaMetArgSerArgProgly 5604
QY 169 CCCCAGTAGA-----AGCTCTCCAGGCGAGCGGTGATCATCGCCCTTCTTGGCTGCCGA 116
Db 5605 AlaAlaSerGlyProAlaSerProGlySerAlaArg---TrpProProArgGlyCysArg 5623
QY 115 ACCACATATGGCGGAGAGCGGTGAGTTCATCTTCATCTGCTGAGTGTGAGTCTTCCCA 56
Db 5624 ArgSer-----SerArgCysThrAlaValThrSerArgCysSerArgArgAlaSerPro 5641
QY 55 GGG 53
Db 5642 Gly 5642

RESULT 14
US-10-118-495-3
; Sequence 3, Application US/10118495
; Publication No. US20030074688A1
; GENERAL INFORMATION:
; APPLICANT: Benning, Christoph
; APPLICANT: Riekhof, Wayne
; TITLE OF INVENTION: Compositions and Methods for the Production of Betaine Lipids
; FILE REFERENCE: MSU-06897
; CURRENT APPLICATION NUMBER: US/10/118,495
; PRIOR FILING DATE: 2002-04-08
; PRIOR APPLICATION NUMBER: 60/283,812
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 416
; TYPE: PRT
; ORGANISM: Rhodobacter sphaeroides
US-10-118-495-3

Alignment Scores:
Pred. NO.: 6.82e-15 Length: 416
Score: 379.50 Matches: 127
Percent Similarity: 43.1% Conservative: 68
Best Local Similarity: 28.1% Mismatches: 182
Query Match: 10.5% Indels: 75
DB: 4 Gaps: 20

US-10-620-914-44 (1-1947) x US-10-118-495-3 (1-416)

QY 691 ACCCAGGGTTCATCCCTACGTGCGGGTGGCGGCCGCCCTACTACTAGTGTGATTGGC 750
Db 2 ThrGlnPheAlaLeuThrHisLeuPro-----AlaProPro-----Valala 15

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QY 751 CGCTGTCCCGCAGCGTGTGGCCACGCGCTGTGCAC-----GAGAGCGCG 789
Db 16 Arg-----GlnIleGlyAlaAlaValHisArgThrSerLeuLeuSerAlaGlyLeu 33
QY 790 GTGAGCGCGCCCGCATGTCTCCCGCCACCTTC-----CTGTACACGAGTCGTGG 840
Db 34 MetGluArg-----MetPheSerArgLeuPheHisGlyLeuValTyProGlnIleTrp 51
QY 841 GAGGACCCCGAGCCCGATATGGAGTGTATGAGATCAACCCCAAGGACACGCGTGTGCAC 900
Db 52 GluAspProAlaValAspMetAlaAlaLeuAlaIleArgProGlyAspArgLeuValAla 71
QY 901 CTGACTAGCGCGCGCTGCAATGCCCTCGAACCTGTGTGTGAGGGGGCGCGCAGGTGGTG 960
Db 72 IleAlaSerGlyGlyCysAsnValLeuSerTyLeuThrGlnGlyProGlySerIleLeu 91
QY 961 TCGGTGAGACTCAACCCCGCGCAGTCGGCGCTTCTGGAGCTGCAAGAAGTGGCCATTCCAG 1020
Db 92 AlaValAspLeuSerProAlaHisValAlaLeuGlyArgLeuLysLeuAlaAlaArg 111
QY 1021 CAGCTG---GAGTTTGAGGCGTGTGGCAdTGTTCGGCGGAGGCGTGCACCCGCGCAT 1077
Db 112 ThrLeuProAspHisAlaAlaPhePheAspLeuPheGlyArgAlaAspLeuProGlyAsn 131
QY 1078 GAGGAGCTGTACGAGAAGAAGCTGGCGCCTTCTCTGTCGCAAAACCCAGCCAACTTCTGG 1137
Db 132 AlaAlaLeuTyArgAspHisIleAlaProAlaLeuAspGlyArgSerArgArgTyTrp 151
QY 1138 -----TCCAAGCGCTCTGGTACTTCCAGCAGCGCTGTACTTACCAG 1179
Db 152 GluAlaArgSerProPheGlyArgGileGlnLeuPheGluArgGlyPheTyArgHis 171
QY 1180 GCGCGCATGGCAAGCTGTGTGGTGTCTdCAGTCCCTGGCGCTGTGTGGAGCTGGCG 1239
Db 172 GlyAlaLeuGlyArgPheIleGlyAlaAlaHisThrLeuAla-----ArgAlaAlaGly 189
QY 1240 AAGACCGTCAAGCGCTCGCAACCGCCCAATGAGAGAGCAGCGCGTGTGTGGGAC 1299
Db 190 ThrAspLeuArgGlyPheLeuAspCysProAspIleGluAlaGlnArgSerPhePheTy 209
QY 1300 AGCAACATGCTCATCCACTTCTGTGAAGAACCGGCCCAAGCGCTGTGTGGTGTGTCTC 1359
Db 210 AlaHisIle-----GlyPro-----LeuPheGlu 217
QY 1360 AAGTTCTGAGCTGTGTCTTCAACAACdCGCTGTGTGTGTGGCGCGCGTGTGGCG 1419
Db 218 AlaProValValGlnAlaLeuAlaArgArgProAlaAlaLeuPheGlyLeuGlyIlePro 237
QY 1420 GCGAAGCAGTACGCGCTGATCAAGCGGAGCGC-----ATCCCATTTGAGAAC 1467
Db 238 ProAlaGlnTyAlaLeuLeuAlaGlyAspGlyAspGlyAspValLeuProVal----- 255
QY 1468 TACATCGCGCGCACCATGGAGCGGTGGCGAGAACTCGCAC----- 1509
Db 256 -----LeuArgGlnArgLeuHisArgLeuLeuCysAspPhe 267
QY 1510 GTGCGCAAGCAGAACTACTTCTACTACAACCTGTCTCACCGGCAAGTTCTCTCGCGACAAC 1569
Db 268 ProLeuArgGluAsnTyPheAlaPheGlnAlaIleAlaArgArgTyProArgProGly 287
QY 1570 -----TGCCCCACTACCTCGCGAGCGCGCTTTCGCCACCTCAAGAGTGGCGTG 1620
Db 288 GluGlyAlaLeuProProTyLeuGluProThrAlaPheGluThrLeuArgGluAsn--- 306
QY 1621 GTGACAACTGACCGCTCTCCCAACTTCTTCATGGAGGAGCTCAAGCGCGCACCTAC 1680
Db 307 AlaGlyArgValGlnIleGluAsnArgSerLeuThrGluAlaLeuAlaAlaGluProGlu 326
QY 1681 ACCAAGGTG-----ATTCTGATGACACCACTGTGAGCTGGCTGATATCCCGTGCGC 1731
Db 327 GluSerIleHisGlyPheThrLeuLeuAspAlaGlnAspTrpMetThrAspAlaGlnLeu 346
QY 1732 AACGAGCTGGCCGAGTGCCTGGCCCAAGCAGGTGTGGCGCGCGGCATCGTCTATCTGGCGC 1791

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Db      347 ThrAlaLeuTrpArgGlnValThrArgThrAlaAlaProGlyAlaArgValIlePheArg 366
Qy      1792 -----TCCGGCTCCCTCAGCGCGCCCTACGCGGAGTGATCCAGAGCGGGGCTTC 1842
Db      367 ThrGlyAlaAlaAspLeuLeuPro-----GlyArgValProGluGluIleLeuGly 384
Qy      1843 GACGTGGCTCATCCCGCGCCCACTCAGGCG-----TACATGGACCGGTCAACATG 1896
Db      385 HisTrpArgAlaAspArgAlaAlaGlyGlnAlaGlyHisAlaAlaAspArgSerAlaIle 404
Qy      1897 TACAGCTCCTTCTACATGGCGCGCGGAGAGGCGCC 1932
Db      405 TyrGlyGlyPheHisLeuTyrArgArgAspAla 416

RESULT 15
US-10-620-914-3
; Sequence 3, Application US/10620914
; Publication No. US20040093639A1
; GENERAL INFORMATION:
; APPLICANT: Benning, Christoph
; APPLICANT: Riekhof, Wayne
; APPLICANT: Klug, Rouven
; TITLE OF INVENTION: Compositions and Methods for the Production of Betaine Lipids
; FILE OF INVENTION: MSU-07769
; CURRENT APPLICATION NUMBER: US/10/620,914
; CURRENT FILING DATE: 2003-07-16
; PRIOR APPLICATION NUMBER: 10/118,495
; PRIOR FILING DATE: 2002-04-08
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 416
; TYPE: PRT
; ORGANISM: Rhodobacter sphaeroides
US-10-620-914-3
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Alignment Scores:
Pred. No.: 6.82e-15 Length: 416
Score: 379.50 Matches: 127
Percent Similarity: 43.1% Conservative: 68
Best Local Similarity: 28.1% Mismatches: 182
Query Match: 10.5% Indels: 75
DB: 4 Gaps: 20

US-10-620-914-44 (1-1947) x US-10-620-914-3 (1-416)
Qy      691 ACCCAGGTTCCATCCCTAGTGCCTGGTGGCGCGCCCTACTAGCTGGATTGGC 750
Db      2 ThrGlnPheAlaLeuThrHisLeuPro-----AlaProPro-----ValAla 15
Qy      751 GCGCTGCCAGCGTTGGCCAGCGCTTGAC-----GAGGAGCGC 789
Db      16 Arg-----GlnIleGlyAlaAlaValHisArgThrSerLeuLeuSerAlaGluGlyLeu 33
Qy      790 GTGAGCGCGCGCCATGTTCCCGCCACCTTC-----CTGTACACGAGTCGTGG 840
Db      34 MetGluArg-----MetPheSerArgLeuPheHisGlyLeuValTyrProGlnIleTrp 51
Qy      841 GAGGACCCCGAGCGGATATGAGTGATGATCAACCCCAAGGACACCGTGTGACC 900
Db      52 GluAspProAlaValAspMetAlaAlaLeuAlaIleArgProGlyAspArgLeuValAla 71
Qy      901 CTGACTAGCGCGGTGCAATGCGCTGAACCTGTGTGAGGGGCGCGCGGTGTGTG 960
Db      72 IleAlaSerGlyGlyCysAsnValLeuSerTyrLeuThrGlnGlyProGlySerIleLeu 91
Qy      961 TCGGTGAGCTCAACCCCGCGCGCTTCGTGGAGCTGAAGAGGTGCCATTTCAG 1020
Db      92 AlaValAspLeuSerProAlaHisValAlaLeuGlyArgLeuLysLeuAlaAlaArg 111
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Search completed: May 5, 2006, 08:02:11
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Qy      1138 -----TCCAGCGCTCTGGTACTTCCAGCAGCGCTCTTACCAG 1179
Db      152 GluAlaArgSerProPheGlyArgArgIleGlnLeuPheGluArgGlyPheTyrArgHis 171
Qy      1180 GCGCGCATGGCAAGCTGTGCTGGTGTGCTGAGTCCCTGCGCGGTGGTGGCTGGCG 1239
Db      172 GlyAlaLeuGlyArgPheIleGlyAlaAlaHisThrLeuAla-----ArgAlaAlaGly 189
Qy      1240 AAGACCTCAGCGCTCGCCAAACGCGCCCAATGGAGGAGCAGCGCGCTGTGGGAC 1299
Db      190 ThrAspLeuArgGlyPheLeuAspCysProAspIleGluAlaGlnArgSerPhePheTyr 209
Qy      1300 AGCAACATGCTCATCCACTTCTCGTGAAGAACCGGCCCAAGCGCTGTGGTGTGCTGTC 1359
Db      210 AlaHisIle-----GlyPro-----LeuPheGlu 217
Qy      1360 AAGTTCGTGAGCCCTGTGCTCTTCAACAGGCCCTGTGCTGTGCGGGCGGTGGCG 1419
Db      218 AlaProValValGlnAlaLeuAlaArgProAlaAlaLeuPheGlyLeuGlyIlePro 237
Qy      1420 GGCAGCAGTACGCGCTGATCAACGCGCGAGCGC-----ATCCCATTTGAGAAC 1467
Db      238 ProAlaGlnTyrAlaLeuLeuAlaGlyAspGlyAspGlyAspValLeuProval----- 255
Qy      1468 TACATCGCGCGCACCATCGCGGTGGCGGAGAACTCGCAC----- 1509
Db      256 -----LeuArgGlnArgLeuHisArgLeuLeuCysAspPhe 267
Qy      1510 GTGCGCAAGCAGAACTACTTCTACAACTGCTCCCGGCAAGTCTCTCGCGGCGAAC 1569
Db      268 ProLeuArgGluAsnTyrPheAlaPheGlnAlaIleAlaArgTyrProArgProGly 287
Qy      1570 -----TCCCGCACCTACCTCGCGGAGCGCGCTTCGCCACCTCAAGAGTGGCGTG 1620
Db      288 GluGlyAlaLeuProProTyrLeuGluProThrAlaPheGluThrLeuArgGluAsn--- 306
Qy      1621 GTGACAACTGACCGTCTCCCAACCTTCTCATGGAGGAGCTCAAAGCGCGCACCTPAC 1680
Db      307 AlaGlyArgValGlnIleGluAsnArgSerLeuThrGluAlaLeuAlaAlaGluProGlu 326
Qy      1681 ACCAAGGTG-----ATTCTGATGACCACTGAGTGGTGGATATGCCCGTGGCC 1731
Db      327 GluSerIleHisGlyPheThrLeuLeuAspAlaGlnAspTrpMetThrAspAlaGlnLeu 346
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Qy      1792 -----TCCGCTCCCTCAGCGCGCCCTTACCCGAGCTGATCCAGAGCGCGGCTTC 1842
Db      367 ThrGlyAlaAlaAspLeuLeuPro-----GlyArgValProGluGluIleLeuGly 384
Qy      1843 GACGTGGCTGCATCGCGCGCGCCACTCAGGCG-----TACATGGACCGGTCAACATG 1896
Db      385 HisTrpArgAlaAspArgAlaAlaGlyGlnAlaGlyHisAlaAlaAspArgSerAlaIle 404
Qy      1897 TACAGCTCCTTCTACATGGCGCGCGGAGGCGCC 1932
Db      405 TyrGlyGlyPheHisLeuTyrArgArgAspAla 416
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GenCore version 5.1.7
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OM nucleic - protein search, using frame_plus_n2p model

Run on: May 5, 2006, 07:53:13 ; Search time 3.9 Seconds
(without alignments)
4621.353 Million cell updates/sec

Title: US-10-620-914-44

Perfect score: 3619

Sequence: 1 atgggtcggtcgctgcagg.....gcgccaaagaaggacaactaa 1947

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Deiop 6.0 , Delext 7.0

Searched: 235405 seqs, 46284737 residues

Total number of hits satisfying chosen parameters: 470810

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-DB=Published Applications AA New -OPWT=fastan -SUFIX=n2p.rapbn -MINMATCH=0.1
-LOOPCL=0 -LOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blomsg2
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -HOST=abs05h
-USR=US10620914 @CNG 1 1 15 @runat 04052006 130718 22549 -NCPU=6 -ICPU=3
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-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications AA New:

1: /SID55/ptodata/1/pubpaa/US08 NEW PUB.pep.*
2: /SID55/ptodata/1/pubpaa/US06 NEW PUB.pep.*
3: /SID55/ptodata/1/pubpaa/US07 NEW PUB.pep.*
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10: /SID55/ptodata/1/pubpaa/US11 NEW PUB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	303.5	8.4	4440	US-10-194-487-525	Sequence 525, App
2	303.5	8.4	4440	US-10-195-883-525	Sequence 525, App
3	303.5	8.4	4440	US-10-195-888-525	Sequence 525, App
4	303.5	8.4	4440	US-10-195-889-525	Sequence 525, App
5	294.5	8.1	386	US-11-096-568A-21828	Sequence 21828, A

6	279.5	7.7	386	11	US-11-096-568A-21828	Sequence 21828, A
7	275	7.6	1886	9	US-10-515-868-8	Sequence 8, Appli
c	270	7.5	495	11	US-11-182-016-31	Sequence 31, Appl
9	267.5	7.4	428	11	US-11-096-568A-19503	Sequence 19503, A
10	267.5	7.4	493	11	US-11-096-568A-11657	Sequence 11657, A
11	267.5	7.4	544	11	US-11-096-568A-19501	Sequence 19501, A
12	267	7.4	1076	9	US-10-131-826A-219	Sequence 219, App
13	267	7.4	1076	9	US-10-973-115B-219	Sequence 219, App
14	267	7.4	1076	9	US-10-137-873A-219	Sequence 219, App
15	267	7.4	1076	9	US-10-152-370-219	Sequence 219, App
16	267	7.4	1076	11	US-11-290-153-219	Sequence 219, App
17	264.5	7.3	1141	11	US-11-217-995-35	Sequence 35, Appl
18	263.5	7.3	1894	9	US-10-134-487-97	Sequence 97, Appl
19	263.5	7.3	1894	9	US-10-195-883-97	Sequence 97, Appl
20	263.5	7.3	1894	9	US-10-195-888-97	Sequence 97, Appl
21	263.5	7.3	1894	9	US-10-195-889-97	Sequence 97, Appl
22	262.5	7.3	1141	11	US-11-217-995-36	Sequence 36, Appl
23	262.5	7.3	1742	11	US-11-182-016-23	Sequence 23, Appl
24	262	7.2	413	11	US-11-096-568A-20771	Sequence 20771, A
25	261	7.2	1356	9	US-10-894-592-3	Sequence 3, Appli
26	258.5	7.1	766	11	US-11-096-568A-19864	Sequence 19864, A
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28	256	7.1	1652	11	US-11-241-631-1	Sequence 1, Appli
29	255	7.0	375	11	US-11-096-568A-23618	Sequence 23618, A
c	254.5	7.0	459	11	US-11-096-568A-21887	Sequence 21887, A
31	253	7.0	2508	11	US-11-241-631-7	Sequence 7, Appli
32	253	7.0	2544	11	US-11-241-631-3	Sequence 3, Appli
33	253	7.0	2601	11	US-11-241-631-9	Sequence 9, Appli
34	251.5	6.9	1128	11	US-11-241-631-11	Sequence 11, Appl
35	250.5	6.9	758	11	US-11-096-568A-14593	Sequence 14593, A
c	249.5	6.9	493	11	US-11-096-568A-11657	Sequence 11657, A
c	248.5	6.9	413	11	US-11-096-568A-20771	Sequence 20771, A
c	247	6.8	428	11	US-11-096-568A-19503	Sequence 19503, A
c	246.5	6.8	544	11	US-11-096-568A-19501	Sequence 5, Appli
40	246.5	6.8	1917	11	US-11-241-631-5	Sequence 5, Appli
41	246	6.8	639	9	US-10-915-002-247	Sequence 247, App
42	244.5	6.8	1743	9	US-10-134-487-451	Sequence 451, App
43	244.5	6.8	1743	9	US-10-195-883-451	Sequence 451, App
44	244.5	6.8	1743	9	US-10-195-888-451	Sequence 451, App
45	244.5	6.8	1743	9	US-10-195-889-451	Sequence 451, App

ALIGNMENTS

RESULT 1

US-10-194-487-525
; Sequence 525, Application US/10194487
; Publication No. US20060074226A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zhen
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430R1C312
; CURRENT APPLICATION NUMBER: US/10/194,487
; CURRENT FILING DATE: 2002-07-12
; PRIOR APPLICATION NUMBER: 10/052586
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17

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; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063121
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063486
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 525
; LENGTH: 4440
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-194-487-525

Alignment Scores:
Pred. No.: 3 78e-11 Length: 4440
Score: 303.50 Matches: 130
Percent Similarity: 36.3% Conservative: 52
Best Local Similarity: 25.9% Mismatches: 212
Query Match: 8.4% Indels: 108
DB: 9 Gaps: 17

US-10-620-914-44 (1-1947) x US-10-194-487-525 (1-4440)
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Db 3794 ThrThrThrGlyAlaGlyCysThrAlaThrCysThrThrThrThrThrGlyAlaThrThrCys 3813
QY 527 TTGCGGCTTCTACGTAGCGCGCAAGTACAGACTGCGCCCTGCGCC----- 571
Db 3814 CysThrThrThrThrCysAlaAlaAlaCysCysAlaCysAlaCysThrGlyCysThr 3833
QY 572 -----AGATGCTCTGTGCGCGCGTCTCTCTGCGCATCGATCTCGACATCGACACA 625
Db 3834 ThrThrAlaCysThrGlyAlaAlaCysThrGly-----ThrCysAlaThrCysAlaThr 3851
QY 626 TTGACATCGCGCGCGCGCGCTTCTCTGAGCAGAGCTGGAGCGCGTGTGGGAGC 685
Db 3852 CysThrThrAlaThrAlaCysAlaThrThrThrThrThrThrThrAlaThrAlaCys----- 3869
QY 686 AGAACCCAGGGTTCGATCCCTTACGTGCGCGTGGCGCGCC----- 730
Db 3870 -----ThrCysAlaGlyCysAlaAlaGlyAlaCysAlaAla 3881
QY 731 ---CCTACTAGTGTGATTGGCGCGCTGCGCGCGTGGCGCGCGCTGCGCGCGCGCGCGCG 787
Db 3882 GlyThrThrThrCysThrCysAlaAlaThrGlyCysCysAlaCysThrCysThrThrThrThr 3901
QY 788 GCGTGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 847
Db 3902 ThrThrCysAlaGlyAlaGlyThrThrThrThrThrThrThrThrThrThrThrThrThrThr 3921
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Db 3922 ThrGlyThrAlaAlaGlyAlaThrGlyThrThrThrThrThrThrThrThrThrThrThrThr 3941
QY 908 GCGGCGGCTGAATGCGCTGAACCTGTGTGGTGGCGAGGGCGCGCGCGCGCGCGCGCGCG 967
Db 3941 hrGlyGlyAlaThrAlaAla-AlaCysThrThrThrThrThrThrThrThrThrThrThrThr 3960
QY 968 ACTGCAACCCCGCGAGTTCGCGCTTCTGAGCTGAAGAGGTGGCCATTCAGCAGCTGG 1027
Db 3961 ThrCysThr----- 3963
QY 1028 AGTTGAGGAGCTGTGGAGAGCTGTTCGCGAGGGCGTGCACCCCGCGCATTTAGGAGCTGT 1087
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Db 3983 Thr-----AlaThrCysCysCysAlaCysAlaThrThrGly-----Ala 3995
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QY 1208 TGCAGTCCCTGGCGCTGTGCTGGAGTGGGCAAGACCGTCACGGCTCGCCAAACGGC 1267
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Db 4035 -----AlaThrGlyThrCysThrThrThrAla----- 4043
QY 1328 ACGGGCCCAAGCCGCTGTGTGCTGTCTGCTCAAGTTCGTGAGCGCTGGTCTCT- 1381
Db 4044 -----ThrThrGlyCysAlaThrThrGlyAlaGlyThrCysThrThrCys 4058
QY 1382 TCAACAGGCGGTGCTGTGTGCTGTGCTGTCTGCTCAAGTTCGTGAGCGCTGGTCTCT- 1441
Db 4059 ThrThrAlaThrCysCysAlaAlaThrAlaAlaAlaAlaAlaAlaGlyAla----- 4075
QY 1442 AGCGGACGCGCATCCCATTTGAGAACTACATCGCGCGCACCATGCGCGGTGGCGGAGA 1501
Db 4076 -----ThrAlaThrGlyAlaAlaThrThr----- 4084
QY 1502 ACTGCGACGTGCGCAAGCAGAACTACTTCTACTACAACTGCTCAGCGGCAAGTTCCTG 1561
Db 4085 -----CysCysAlaThrThrAlaThrThrGlyAlaAlaAlaAlaThrCysThrThrCys 4102
QY 1562 GCGACAACTGCGCCACCTACTCTGCGCGAGGGCGCTTGCACCCCTCAAGAGTGGCGTGG 1621
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QY 1622 TGAACAACCTGACCGCTCCACCAACTTCTTCTGAGAGAGCTCAAAAGCGCGCACTACA 1681
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RESULT 2
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; Sequence 525, Application US/10195883
; Publication No. US20060073544A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
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; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C323
; CURRENT APPLICATION NUMBER: US/10/195,888
; CURRENT FILING DATE: 2002-07-15
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 525
; LENGTH: 4440
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-195-883-525

Alignment Scores:
Pred. No.: 3,78e-11 Length: 4440
Score: 130 Matches: 130
Percent Similarity: 36.3% Conservative: 52
Best Local Similarity: 25.9% Mismatches: 212
Query Match: 8.4% Indels: 108
DB: 9 Gaps: 17

US-10-620-914-44 (1-1947) x US-10-195-883-525 (1-4440)
QY 473 ACAAGCTCATCGACGAGCTTGTCTGCTACCTGCTCCAGAGC-----GCCTGTGGGCG 526
DB 3794 ThrThrThrGlyAlaGlyCysThrAlaThrCysThrThrThrThrThrGlyAlaThrThrCys 3813
QY 527 TTGCGGACTTCTACGTGAGCGCGCAAGTACGAGCTGCTCCCTCGGCG----- 571
DB 3814 CysThrThrThrThrThrCysAlaAlaAlaCysCysAlaCysAlaCysThrGlyCysThr 3833
QY 572 -----AGATCGCTGTGGCGCGCTTCTTCTGCGCATGCATCTTCGACATCGACACA 625
DB 3834 ThrThrAlaCysThrGlyAlaAlaCysThrGly-----ThrCysAlaThrCysAlaThr 3851
QY 626 TTGACATCGCGCCGAGCGCGCTACCTGAGCAGCAAGCTGGAGCGCTGTGGGAGC 685
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DB 3870 -----ThrCysAlaGlyCysAlaAlaGlyAlaCysAlaAla 3881
QY 731 ---CCTACTAGTGTGGAGTGGCGCTGCCAGCGTTGGCCAGCGCTGCACGAGGAGC 787
DB 3882 GlyThrThrCysThrCysAlaAlaThrGlyCysCysAlaCysThrCysThrThrThr 3901
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DB 3902 ThrThrCysAlaGlyAlaGlyThrThrThrThrThrThrThrThrThrThrGlyThr 3921
QY 848 CCGAGCGGATATGAGGTGATGAGATCAACCCCAAGGACACGCTGCTGACCTGACTA 907
DB 3922 ThrGlyThrAlaAlaGlyAlaThrGlyThrThrThrThrThrThrThrCys--ThrThrCysT 3941
QY 908 CGCGCGCTGCAATGCCCTGCAACCTGTGGTGGCAGGGGCGCGCCAGGTGTGTGGTGG 967
DB 3941 hrGlyGlyAlaThrAlaAla-AlaCysThrThrThrAlaGlyAlaAlaThrCysAlaCys 3960
QY 968 ACTGCAACCCCGCAGTGTGGCGCTTCTGGAGCTGAAGAAGTGGCCATTCAGCAGCTGG 1027
DB 3961 ThrCysThr----- 3963
QY 1028 AGTTTGAGGAGCTGTGGCAGCTGTTTGGCGAGGGCGTGCACCCGCGCATTCAGGAGCTGT 1087
DB 3964 ---ThrThrThrThrThrCysCysAlaAlaGlyThrAlaAlaAlaAlaAlaThrAla 3982
QY 1088 ACdGAGAAGAGCTGGCGCCCTTCTGTGCGAAACAGCACAACCTTCTGTGTCGAAGCGCC 1147
DB 3983 Thr-----AlaThrCysCysCysAlaCysAlaThrThrGly-----Ala 3995
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DB 4016 CysThrAlaAlaThrThrCysAlaGlyGlyAlaAlaAlaAlaAlaAlaThrGlyThr--- 4034
QY 1268 CCACAATGGAGGAGCAGCGCGTCTGTGGGACACCACTGCTCATCCACTTCGTGAAGA 1327
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QY 1382 TCAACAAGCGCGTGTGTGTGGCGCGCGCGTGGCGGCAAGCAGTACGCGGTGATCA 1441
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DB 4076 -----ThrAlaThrGlyAlaAlaThrThr----- 4084
QY 1502 ACTGCGACGTGCGCAAGCAGAACTTCTACTACAAGTGCCTCACCGGCAAGTTCTCTGC 1561
DB 4085 -----CysCysAlaThrGlyThrAlaThrThrGlyAlaAlaAlaThrCysThrThrCys 4102
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DB 4123 ThrThrThr---CysAlaCysAlaThrGlyThrCysCysThrGlyCysAlaAlaAlaThr 4141
QY 1682 CCAAGTGATTCTGATGACACCGTGGCTGGGATATGC-----CCGTGGCCA 1732
DB 4142 -----GlyThrAlaThrThrGlyThrThrAlaAlaAlaThrThrAla 4156
QY 1733 ACGAGTGGCGGAGTGTGCTGCCAAGCAGGTGCGCGGCGGCGCATCGTCATCTGGCGCT 1792
DB 4157 ThrThrThrThrAlaGlyGlyThrAlaThrThrThrThrThrAlaGlyGlyGlyAla 4176
QY 1793 CGGCTCCCTCAGCGCGCCCTACGCCGAGTGTATCCAGAGGGGGCTTCGACGCTCGCT 1852
DB 4177 AlaAlaThrGlyAlaThrThr-----ThrCysThr 4187
QY 1853 GCATCCGCGCGCCACTCAGCGCTACATGACCGCGTCAACATGTACAGCTCCTTCTACA 1912
DB 4188 AlaAlaGlyThrThrThrGlyThrAlaThrThrThrThrThrThrAlaGlyCysThr 4207

RESULT 3
US-10-195-888-525
; Sequence 525 Application US/10195888
; Publication No. US20060073545A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Deenoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C324
; CURRENT APPLICATION NUMBER: US/10/195,888
; CURRENT FILING DATE: 2002-07-15
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
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Db 55 ArgProGlyProGlyArgAlaProArgGlyAlaAlaGlyProArgArgPro----- 71
Qy 1582 GGTAGTGGGGCAGTTGTCCG----- 1562
Db 72 ---GlyGlyGlySerThrArgSerGlyLeuAlaLeuAlaArgGlnProGlnMetProArg 90
Qy 1561 ---GCAGGAACCTGCGGTGAGGAGGTGTAGTAGAGTAGTCTGCTTGCGCAGCTGCG 1505
Db 91 GlySerGlyAlaSerArgProGlySerCysSer-----SerArgGly 104
Qy 1504 AGTTCTCCGCCACGCGTCCATGTGCGCGGATGTAGTTCTCAATGGGATGCGGTCCG 1445
Db 105 SerThrGlyProArgArg---TipProAla---AlaGlyGlyArgTrp----- 118
Qy 1444 CCTTGATCAGCGGTACTGCTTGCCCGCA-----CGCCGCGCGGAACC 1400
Db 119 -----ArgThrProCysProCysAlaSerProSerProArgAlaArgPro 134
Qy 1399 ACAGCAGCGCTTGTGAAGAGCACCAGGCTCACGAATTGACGACAGCCACACACGCG 1340
Db 135 ThrAlaAlaGlyAlaThrSerThrGlyCys-----SerThrAlaThrAlaAla 151
Qy 1339 ---GCTTGGGCGCTTCTTCAGAGTGCATGATGTCATGCTGTCCTCCACAGCGCGCT 1283
Db 152 ArgThrTrpProArgArgAlaGlyThrGlyCysThrThrCysSerPro----- 167
Qy 1282 GCTCCTCCATTGTGGCGCGTTGGAGCGCTTGACGGTCTTGCCTCCAGTCCGACACCA 1223
Db 168 -----ArgSerSerProLeuProSerPro 175
Qy 1222 -----CGGCCAGGC-----ACTGCAGCACCACGACAGCTGCG 1190
Db 176 ProThrAlaProArgArgProGlyProProArgTrpAsnAlaAlaSerArgGlyTrpThr 195
Qy 1189 CCA-----TGCCGCGCTGTGTAGTACAGCGCGTGTGAAGTACCAGA----- 1148
Db 196 ProArgArgCysArgProAlaGlyAlaProProAlaAlaAlaThrArgThrSerAlaThr 215
Qy 1147 -----GGCGCTTGGACCAGAAAGTTGTGGCTGTGTTTGGCACA 1112
Db 216 ThrTrpAlaProProTrpTrpProSerTrpArgSerAlaAlaSerTrpTrpProThr 235
Qy 1111 GGAAGGGCGCAGCTTCTTCGTACAGCTCCTCAATGC-----GCGGGTGCAGCCCT 1058
Db 236 -----ValAlaThrAlaAlaArgCysAlaAlaGlyAlaAlaArg 249
Qy 1057 GCGCGAACAGCTGCACACGCTCCTCAAACTCCAGCTGCT-----GAATGG----- 1013
Db 250 ArgArgCysArgCysArgArgThrThrSerProThrAlaProThrSerTrpSerGlySer 269
Qy 1012 ---CCACCTTCTTACGTCCAGAGCGCGAGCTGCGCGGGTGTGAGTCCACCGACACCA 956
Db 270 ArgProArgAlaAlaAlaSerSerSerGlyArgAlaAlaArgAlaCysTrpAlaSerSerPro 289
Qy 955 CTGGCGCGCCCTGACACAGCAGGTTCAGGCAATTCAGCCCGCTAGTCAGGCTCA 896
Db 290 -----CysProAlaProSerGlyThrAlaThrSerSerArgThr-----Ser 303
Qy 895 GCACCGTCTCTTGGGGTGTATCTCCATCACCTCCATATCCG-----GCTCGGGTCTCT 842
Db 304 ArgProCysProArgSerArgSerProThrAlaProThrProThrSerAlaSerSerSer 323
Qy 841 CCCAGACTGTGTACAGGAGGTGGCGGGAACATGGCGGGCTCCACGCGCTCTCT 782
Db 324 ProAlaThrAla-----SerGlyThrTrpLeuAlaThr-----ArgPro 336
Qy 781 CGTGAGGGCGTGGCCACGCTGGSCAGCGCGCCCAATCCACAGTAGTAGGGGGCGCGCA 722
Db 337 ArgAla-----ArgTrp-----Arg 341
Qy 721 GCCACGGCAGTAGGGGATCGAACCCCTGG-----TGTTCTGCT 683
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Db 342 AlaProAlaSerAlaGlyGlyProGlyGlyAlaProArgProProArgCysSerPro 361
Qy 682 CCCACACGCGCTCCAGCTTCTGCTCCA 656
Db 362 SerTrpProSerProGlyAlaAlaPro 370
RESULT 6
US-11-096-568A-21828
; Sequence 21828, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; TITLE OF INVENTION: Therby
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 21828
; LENGTH: 386
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(386)
; OTHER INFORMATION: Ceres Seq. ID no. 12406424
US-11-096-568A-21828
Alignment Scores:
Pred. No.: 8,46e-10 Length: 386
Score: 279.50 Matches: 126
Percent Similarity: 36.4% Conservative: 31
Best Local Similarity: 29.2% Mismatches: 123
Query Match: 7.7% Indels: 151
DB: 11 Gaps: 22
US-10-620-914-44 (1-1947) x US-11-096-568A-21828 (1-386)
Qy 711 CGTCCGCTGCTGCGCGCCCTACTACTGTTGGATTGGCGCTGCCAGCGTTGGCCA 770
Db 37 ArgCysAlaAlaThrArgProGlnArgHisArgTrpProAspArgArgArgPro 56
Qy 771 CGCCCTGCACGAGGCGCGTGGAGCGCGCCCATGTTCCCGCCACCTTCTCTGTACAC 830
Db 57 GlyProGlyArgAlaProArgGlyAlaAla----- 66
Qy 831 GCAGTCTGGGAGAGACCCCGAGCCGGATATGGAGGTATGAGATCAACCCCAAGGACAC 890
Db 67 -----GlyProArgArgProGlyGlySerThr----- 76
Qy 891 GGTCTGACCTGACTAGCGCGGCTG-----CAATGCCCTGAA 929
Db 77 -----ArgArgLeuLeuAlaAlaArgGlnProGlnMetProArg 90
Qy 930 CCTGCTGTTGCGGGGCGCGCCAGGTGTTGCGTGGACTGCAACCCCGCAGTCGCG 989
Db 91 GlySerGlyAla---SerArgProGlySerCysSer-----SerArgGly 104
Qy 990 GTTCTGGAGCTGAAGAAGTGGCCATTCACAGCTGAGTTTGAGACGTGTGCGACGT 1049
Db 105 SerThrGlyPro---ArgArgTrpProAlaAlaGlyGlyArgTrpArgThrProCysPro 124
Qy 1050 GTTCGGCGAGGCGTGCACCGCGCATTTGAGGAGCTGTACGAGAAGAAGCTGGCGCCCTT 1109
Db 124 ysAlaSer-----ProS 128
Qy 1110 CCTGTCGCAACACAGCCCAACTTCTGTTCCAGCGCTCTGGTACTTCCAGACGCGCT 1169
Db 128 erProArgArgAlaArgProThr-----AlaAlaGlyGlyAlaThrSerThrGlyC 145
Qy 1170 GTACTACAGGCGCGCA-----TGGCGCAAGCTGTGCTGGGTGC---TGCAGTGCT 1217
Db 145 ysSerThrAlaThrAlaAlaArgThrTrpProArgArgAlaGlyThrGlyCysThrThr- 164
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QY 1218 GGCCGTGTGTGGGACTGGGCAAGACCGTCAAGCGCTCGCCCAACGCGCCCAATGGA 1277
Db 165 -----CysSerProArgSerProLeuProSerProProThrAlaProArg----- 180
QY 1278 GGAGCAGCGCGTCTGTGGGACAGCAACATGCTCATCTCGTGAAGAGCGGCCAA 1337
Db 181 -----ArgProGlyProp 185
QY 1338 GCCGTGTGTGTGGTTCGTCAAGTTCGTGAGCCTGGTGTCTTCAACAAGGCGGTCT 1397
Db 185 roArgTrp-----AsnAlaAlaSerArgGlyTrp-----ThrProArgArgC 199
QY 1398 GTGGTTCGGCGCGGTGGCGGCAAGACGATGACGCGTGTATCAAGGCGGACGCGATCCC 1457
Db 199 ysArgProAlaGlyAlaProProAlaAlaAlaThrArgThrSerAlaAlaThrTrpAlap 219
QY 1458 CATTGAGAACTACATCGCGCGCACCATGAGCGCGGTGGCGGAGAACTCGCAGTGGCAA 1517
Db 219 ro-----ProProTrp-----TrpProSerTrpArgSerAlaAlas 231
QY 1518 GCAGAACTACTTCTACTACAACTGCTCACCGGCAAGTTCCTGCGCGCACAACTGCCCCAC 1577
Db 231 erTrpTrpProThrValAlaThrAla-----AlaArgCysCysAlaAlaGlyAla 247
QY 1578 CTACCTGCGGAGCGGCGCTTGGCCACCCTCAAGAGTGGCGGTGGGAAACCTGACCGT 1637
Db 248 -----AlaArgArgArgCysArgCysArgArg-----ThrThrSerProT 261
QY 1638 CTCACCAACTCTTCTATGAGGAGCTCAAGCGCGCACCTACACCAAGGTGATCTGAT 1697
Db 261 hrAlaProThrSer----- 265
QY 1698 GGACCACGTGACTGGCTGGATATGCTCGCGTGGCCAAAGAGTGGCGAGTGGCTGGCCAA 1757
Db 266 -----TrpSerGly-----S 269
QY 1758 GCAGTTGCGCGGCGCGCATGTCATCTGC----- 1789
Db 269 erArgProArgAlaAlaAlaSerSerSerGlyArgAlaArgAlaCysTrpAlaSerSerP 289
QY 1790 --GCTCGCTCCCTCAGCCCGCTCAGCGAGCTGATCAGAGCGGCGGCTTCGAGT 1847
Db 289 roCysProAlaProSerGlyThrAlaThrSerSerArgThrSerArgProCysProArgs 309
QY 1848 GCGTGTATCCGCGCGCACTCAGGCGTACATGGACCGCTCAACATGTACAGTCTCCT 1907
Db 309 erArgSerProThrAlaProThrProThrSerAlaSerSerSerProAlaThrAlaSerG 329
QY 1908 CTACATGCGCGCGGAGGCGGCCAAGA 1936
Db 329 lyThrTrpLeuAlaThrArg--ProArg 337

RESULT 7
US-10-515-868-8
; Sequence 8, Application US/10515868
; Publication No. US20050282729A1
; GENERAL INFORMATION:
; APPLICANT: Hamilton, David W
; APPLICANT: Roberts, Kenneth P
; APPLICANT: Enerud, Kathy M
; TITLE OF INVENTION: CRISP POLYPEPTIDES AS CONTRACEPTIVES AND INHIBITORS OF SPERM
; TITLE OF INVENTION: CAPACITATION
; FILE REFERENCE: 110.01860101
; CURRENT APPLICATION NUMBER: US/10/515,868
; CURRENT FILING DATE: 2004-11-24
; PRIOR APPLICATION NUMBER: 60/383,628
; PRIOR FILING DATE: 2002-05-28
; PRIOR APPLICATION NUMBER: PCT/US03/16669
; PRIOR FILING DATE: 2003-05-28
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 8
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; LENGTH: 1886
; TYPE: PRT
; ORGANISM: HOMOSAPIEN
US-10-515-868-8
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Alignment Scores:

Pred. No.:	1.91e-09	Length:	1886
Score:	275.00	Matches:	133
Percent Similarity:	33.4%	Conservative:	52
Best Local Similarity:	24.0%	Mismatches:	222
Query Match:	7.6%	Indels:	147
DB:	9	Gaps:	17

US-10-620-914-44 (1-1947) x US-10-515-868-8 (1-1886)

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QY 473 ACAACGTATCATGACACCGCTGTCTGTACCTGTCCCAAGACGGCTGTGGCGTGGCCG 532
Db 993 ThrThrThrCysThrThrAlaGlyThrGlyCysThrGlyGlyAlaGlyThrAlaAla 1012
QY 533 ACTTCTACGTGAGCGGCAAGTACGACCTGCCCTCGCGCCAGATCCCTGTGGCGCGCT 592
Db 1013 AlaGlyGlyThrCysAlaAlaGlyThrCys---CysAlaAlaCys-----AlaCys 1028
QY 593 TCTTCTGGCGATCGATCTTCGACATCGACACATTTGACATCGCGCCGAGCGCGCGCT 652
Db 1029 CysThrGlyCysCysThrThrAlaAlaAlaThrThrAlaAlaAlaThrCysAlaThr 1048
QY 653 ACCTGGAGCAGAACTGGAGCGGTGGGAGCAGACACCCAGGTTCCGATCCCTACG 712
Db 1049 GlyThrGlyAlaThrThrAlaAlaThrAlaGlyThrThrThrThrAlaAlaGlyThr 1068
QY 713 TGGCGTGGTGGCGCGCCCTACTACG----- 739
Db 1069 ThrGlyGlyCysAlaThrAlaAlaThrThrCysAlaAlaCysThrThrAlaThrGlyGly 1088
QY 740 -----TGTGATTTGGCGCGCTGCCA 760
Db 1089 ThrAlaThrAlaAlaCysThrGlyGlyThrCysCysCysThrCysAlaAlaCysAla 1108
QY 761 GCGTTGGCCAGCGCTCGACGAGGAGCGCTGGAGCGCGCGCCCATGTTCCCGCCCACT 820
Db 1109 GlyThrAlaAlaCysCysThrGlyGlyCysThrAlaAlaAlaAlaAlaThrAlaGlyGly 1128
QY 821 TCCTGTACAGCAGTCTGTGGAGGAGACCCCGAGCCGGATATGGAGGTGATGGAGATCAAC 880
Db 1129 ThrCysThrThrAlaThrGly-----Thr 1136
QY 881 CCAAGGACAGGTGCTGACCTGACTAGCGCGCTGCAATGCTGCACTGCTGCTGCTGTC 940
Db 1137 GlyGlyThrThrCys-----AlaAlaCysThrCysCysCysAlaCysCysCys 1153
QY 941 AGGGGCGCGCCAGGTGGTGGTGGAGTCAACACCGCGCGAGTGGCGCTTCTGGAGC 1000
Db 1154 CysGlyCysCysThrThrCysCysCysCysAlaThrAlaThrThrThrCysAlaAla 1173
QY 1001 TGAAGAGGTGGCCATTCAGCAGCTGGAGTTTGAGGACGTGTGGCAGC----- 1048
Db 1174 CysCysAlaCysThrCysThrGlyAlaThrAlaThrCysThrCysThrCysCysThr 1193
QY 1049 ---TGTTCGGGAGGCGGTGACCCCGCGCATTTGAGGAGCTGT-----ACGAGAGA 1096
Db 1194 GlyCysAlaCysAlaAlaCysThrAlaAlaCysAlaThrCysCysAlaGlyThrAlaAla 1213
QY 1097 AGCTGGCGCTTCTCTGTCGCAACACAGCCACAACTTCTGCTCAAGCGCTCTGGTACT 1156
Db 1214 ThrAlaAlaThrThrCysThrThrCysAlaCysThrThrThrThrAlaAlaAlaThr 1233
QY 1157 TCCAGACGCGCTGTACTACAGCGCGCATGGGCAAGCTGTGCTGGTGTGTCAGTGCC 1216
Db 1234 ThrThrThrAlaCysThrThr-----CysThrAlaCysThrThrThr 1247
QY 1217 TGGCGTGGTGGGACTGGGAGACCGTCAAGCGCTCGCCCAACGCGCCCAATGG 1276
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Db 1247 ----- 1247
QY 1277 AGGACACCGCGTCTGGGACAGCAACATCTCATCCACTTCTGTGAAGAACGGGCCCA 1336
Db 1248 ---AlaAlaAlaThrCys---AlaAlaThrCysAlaThrThrAlaAlaAlaGlyGlyAla 1265
QY 1337 AGCGCGTGGTGGTGTCTGTCAGTTCGTGAGCC----- 1372
Db 1266 AlaThrCysCysAlaCysAlaAlaAlaGlyCysAlaAlaAlaCysAlaGlyAlaGlyThr 1285
QY 1373 TGGTCTCTTCAACAGCCCGTGTGTGTTCGGCGCGCGTGTGGCGGCAAGCAGTACG 1432
Db 1286 ThrCysAlaGlyThrCysThrCysAlaThrThrAlaAlaAlaGlyCysAlaGlyGlyThr 1305
QY 1433 CGTGTATCAAGCGGACGGCATCCCATTTGAGAACTACATCG----- 1474
Db 1306 ---AlaAlaAlaThrAlaThrCysAlaThrThrAlaAlaAlaThrThrGlyGlyAla 1323
QY 1475 ---CGCGCACCATGACGCGGTGGCGGAGAACTCGCAGTGGCGCAAGCAGAACTACT 1528
Db 1324 AlaGlyThrAlaGlyThrThrAlaAlaAlaThrAlaAlaAlaThrCysThrCysAlaThrThr 1343
QY 1529 TCTACTACAACTGGCTACCGCGCAAGTTCCTGCGCAACAACTGGCCCACTACCTACCTGCGCG 1588
Db 1344 GlyThrThrThrAlaThrThrAlaThrThrGlyAlaCysAla-----CysAla 1357
QY 1589 AGGCGGCTTCGCCACCTCAAGAGTGGCGGTGGAGCAACTGACCGTCTCCACCAACT 1648
Db 1358 ThrCysThrAlaThrAlaThrAlaThrAlaCysAlaThrThr----- 1371
QY 1649 TCTTCATGAGGAGCTCAAGCGCGCACCTACACCAAGTGTATTCGATGGACCACTGGG 1708
Db 1372 -----ThrGlyThr-Gl 1375
QY 1709 ACTGCTGGATATGCCGTGGCAACAGCTGGCGAGTGGCTGGCCAAAGCAGGTGGCG 1768
Db 1375 yAlaAlaGlyCysAlaAlaGlyAlaAlaAlaCysAlaAlaThrAlaAlaAlaAlaAla 1395
QY 1769 CGGCGGGCATGTATCTGGGCTCCGCTCCCTCAGCGCCCGCTACGCGCGAGCTGATCC 1828
Db 1395 agly--CysThrThrCysGlyThrAlaThrGlyCysCysAlaThrThr----- 1410
QY 1829 AGAAGCGGGCTTCGACGTGGCTGCATCCGCGCGCCACTCAGGGCTACATGACCGCG 1888
Db 1411 -----AlaAlaThrThrAlaAlaAlaCysAlaAlaAlaAlaAlaThrAlaThrGlyThrAla 1428
QY 1889 TCACATGT-----ACAGTCTCTTCT 1909
Db 1429 ThrThrCysAlaGlyThrAlaCysThrGlyAlaThrThrGlyCysAlaThrAlaCysAla 1448
QY 1910 ACATGGCGCGCGGAGGGCGCAAGAGGAACT 1945
Db 1449 AlaGlyAlaThrGlyCysAlaThrGlyThrThrThr 1460

RESULT 8

US-11-182-016-31
; Sequence 31, Application US/11182016
; Publication No. US20060019294A1
; GENERAL INFORMATION:
; APPLICANT: SUGEN, INC.
; TITLE OF INVENTION: TYROSINE KINASE SUBSTRATE (TKS) PROTEINS
; FILE REFERENCE: 038602/0102
; CURRENT APPLICATION NUMBER: US/11/182,016
; PRIOR FILING DATE: 2005-07-15
; PRIOR APPLICATION NUMBER: US/09/958,359
; PRIOR FILING DATE: 2002-02-05
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 31
; LENGTH: 495
; TYPE: PRT
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Tks 118
US-11-182-016-31
Alignment Scores: 3.32e-09 Length: 495
Pred. No.: 270.00 Matches: 150
Score: 270.00 Conservative: 40
Percent Similarity: 30.7% Mismatches: 171
Best Local Similarity: 24.3% Indels: 257
Query Match: 7.5% Gaps: 34
DB: 11
US-10-620-914-44 (1-1947) x US-11-182-016-31 (1-495)
QY 1811 GCGCGGCTGAGGAGCGGAGCGCCAGATGAGATGCGCCCGCGCAACTGCTTG--- 1755
Db 2 GlyGlyCysArg-----LysAspValTrpLuserProGlyHisCysCysileTrp 18
QY 1754 -----GCCAGGCACCTCGCCAGCTCGTTGGCCACCGGC----- 1722
Db 19 GlyAspArgLeuSerLeuProSerArgGluProGlyLeuIleLeuThrGlyGlyPro 38
QY 1721 -----ATATCCAGCCAGTCCAGGTGGTCCATCAGATCACGATCACCTTG 1683
Db 39 IleProGlyArgValLeuAsnValAsnSerGlnAla----- 50
QY 1682 GTGTAGTGGCGCGCTTTCAGTCTCCATGATGAAGATTGGTGGAGACGGTCAGGTGTGCC 1623
Db 51 -----SerSerSerSerAsnLysGluAlaMetSerGluArgGlyArg 64
QY 1622 ACCACGCCACTCTTGGAGTGGCGAAGCGCCCTCGCGCAGGTAGTGGTGGGCGAGTTGTCG 1563
Db 65 AlaArgCysAlaLeuSerLeuThrGlnAla-ProArgSer-----Trp----- 78
QY 1562 CGCAGGAACCTTCCGCGTGGAGCAGTTGTAGTAGAAGTAGTCTCTGCGCAGCAGTGGCAG 1503
Db 79 -GlnGlyThrCysGlnAsnGlyHisProAlaHisSerHisAlaThrSerLeuArgSe 98
QY 1502 TTCTCCCGCAGCGCTCCATGGTGGCGCGATGTAGTTCTCAATGGGATGCCGTCGCC 1443
Db 98 f-----ProArg----- 100
QY 1442 TTGATCAGCGGTACTCTTTCGCCGCGACCGCGC-----CGCCGAACACAGCAGCGCC 1389
Db 101 -----CysProGlySerArgGlyGlnArgArgSerLeu----- 111
QY 1388 TTGTTGAAGACACAGGCTCAGAACTTGACGAACACACACAGCGCGCTTGGGCGCG 1329
Db 112 -CysArgArgLeuProGlySerArgThrGlyHisGlyHisArgAlaLeuAlaHisAlaPr 131
QY 1328 TTCTTCACGAAGTGCATGTCGTGTGCCACAGCGCGCTCTCTCCTCCTCATTGTG 1269
Db 131 oGlyProGluCysGlyGlnCysAlaGlnSerGlnHisLeuAlaAlaAlaProValGl 151
QY 1268 GCGCGTGGCGAGCGCTTGACCGTCT----- 1241
Db 151 yAlaAlaArgArg-----ArgSerProAlaLeuGluValProHisThrGlnProPr 168
QY 1240 -----TGCCAGTCCCAGCACCGG----- 1220
Db 168 oLeuLeuProAlaProAspMetGluGluCysTrpAlaProAlaProGlnGlnGlyAspLe 188
QY 1219 -CCAGGCACCTGACAGCCAGCAGCTTGGCCATGCGCCCTGGTAGT---ACAGGCGCG 1164
Db 188 uProTrpAlaLeuArgTrpGlnGlnLeuAlaLeuCysGlnSerGlySerLeuValGlyAl 208
QY 1163 TGCTGGAAGTACCAGAGCGCT-----TG 1140
Db 208 aAlaSerAlaGlyArgGlySerSerAlaCysGlnAlaGluAspTrpArgTrpArgTrpTr 228
QY 1139 GACCAAGAGTGTGGCTGG---TTTGGACAGGAAGGCGCGCAGCTTCTTCGTACAGC 1083
Db 228 pThr-----TrpProSerProSerAlaLysSerProSerGlyAlaAlaGlnTh 244

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QY 1082 TCCT-----CAATGCGCGG 1068
Db 244 rProAlaHispeGlySerLeuLysProLeuLeuAlaAlaProThrSerCysSerG1 264
QY 1067 TGCAGCCCTCGCCGACAGCTGCCACAGCTCTCAACTCCAGCTGCTGAATGCCAC 1008
Db 264 yGlyTrpProArgHisProAla-----ProAspSerAlaAlaProGlyValGlnPr 281
QY 1007 T-----TCTTCAGCTCCAGAGCCGCTGCGCGGGTTGTCAGTCCACCCAGCACACC 954
Db 281 oHisAlaAlaHisAlaProGlyAlaProAlaProAlaAlaValProProArgProAl 301
QY 953 TGGCCGCGCCCTGCA----- 938
Db 301 aAlaPheProAlaAspGlySerProProSerLeuLeuTrpProArgSerCysLe 321
QY 937 -----CCAGCAGGTTTC 927
Db 321 uTrpGlnProPheSerGlnThrArgHisTrpSerSerGlyThrGlnSerProLeuGlyPr 341
QY 926 AGGCATTGCAGCCCGCTAGTCAGGGTTCAGCACCGTGT----- 887
Db 341 oGly---ValProArgProGlySerGlyHisSerProCysGluSerCysSerTrpHisLe 360
QY 886 ---CCTTGGGTTGATCT-----CCATCACTCCATATCCGGTCCGG-- 848
Db 360 uLysProTrpProProSerProCysThrGlnAlaProHisProProArgProValArgTr 380
QY 847 ---GGTCTCCACAGCTCGGTACAGGAAGTGGCGGGAACATGGCGGCGCG 795
Db 380 pSerHisGlyProProSerGlySerTrpPro-----TrpCysArgGlyTrpHisArgLe 398
QY 794 TCCAGCGCT-----CCTCGTCGAGGGCTGCCCAACGCTGGCGAGCGGCCA 747
Db 398 uProSerAlaHisArgSerArgProArgLeuSerSerGlyGlnLeuTrpAla----- 415
QY 746 ATCCACAGTAGTAGGGCGCGCAGCCAGCCAGTAGGAGATCAACCTCGGTGTTC 687
Db 416 ---ValGlnSerTrpGly---ProSerLeuCysArgArgArgTrpSerProSerArgCy 433
QY 686 TGCTCCACACAGCGCTCCAGCTTCTGCTCCAGTAGGCGCGCTCGGGCCGATGTCA 627
Db 433 sAlaProProProSerProProGlyHisProProLeuCysGlnProArgGly---CysHi 452
QY 626 ATGTTGTGATGTCGAGATCGATCGCCAGAGAAACGCGCGCACCGGCATCTGGCGC 567
Db 452 sCysCys----- 454
QY 566 AGGGCAGGTGCTACTTCGCGCTACGTAGAGTCGGCAACGCCACCGCGCTCTTGG 507
Db 455 -----CysLeuHisArgArgGluProSerArg----- 463
QY 506 GACAGGTACGACAGCTGCTGATGATGCTGTGGAACGGTGGNAATCATCGTGGCGAG 447
Db 464 -SerGlyThrSerArgPro----- 469
QY 446 TAGGAGAAGGTGATGAGCGTCCGCTGCGCTCAGGGGCGCAAAATTTGCAAGCGTCGGCC 387
Db 470 -----ProAlaArgArgPr 474
QY 386 T-----CCACGACCTGGACATTCCTTCAGCCCTTGGGCTTCGCT 347
Db 474 oLeuAlaAlaLeuAlaArgSerGlySerProProTrpProAlaPro 491
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RESULT 9

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US-11-096-568A-19503
; Sequence 19503, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nickolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; TITLE OF INVENTION: Thebdy
; FILE REFERENCE: 2750-1592PUS
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; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 19503
; LENGTH: 428
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(428)
; OTHER INFORMATION: Ceres Seq. ID no. 12373378
US-11-096-568A-19503

Alignment Scores:
Pred. No.: 4,65e-09 Length: 428
Score: 267.50 Matches: 126
Percent Similarity: 41.6% Conservative: 30
Best Local Similarity: 33.8% Mismatches: 103
Query Match: 7.4% Indels: 116
DB: 11 Gaps: 30

US-10-620-914-44 (1-1947) x US-11-096-568A-19503 (1-428)
QY 205 CGCTCGAACCTCATCTGGTTGACCTGGTGGT---GGCACTGGGGAGAAATGTCATATG 261
Db 131 ArgGlyAsnIleLeuSerTyrAsnLeuGlyGlyHisGly-LeuGlnArg----- 146
QY 262 ATGGCTGATTACATCGACCTGGCGAAGTTCAAAGTCCATCTACGTGG---TCGACCTGTGC 318
Db 147 -----ArgAlaSerSerProSerIleTrpProAlaThrCysSe 159
QY 319 CACTCGCTGTGCGAGGTGGCCAGAAAGGCGCAAGGCGTGGAAATGTCGAC 378
Db 159 r-----ArgProAlaAla-----Ar 164
QY 379 GTCGTGAGGCGCAGCTTGCCATTTCGCCCTTGGGCGACGCGCAGCTCATACC 438
Db 164 gAlaTrp---ProTrpTrpSerAlaArgPro-----SerProSerArgGlyThrPr 181
QY 439 T-----TCTCTACTCGCTCACGATdTATCCCGTTCACACGCTCATCGACCAG 489
Db 181 oGlySerGlyAlaProCysSerSerArg-----ThrProSerSerGlyPr 196
QY 490 GCTTGTCTGACTCTGT-----CCCAAGACGCG 516
Db 196 oAlaAlaArgArgCysCysProThrGlyAlaAlaThrSerThrAlaProSerThrSe 216
QY 517 CTGG-----TGGCGTTGCGGACTTCTACGTGAGCGGCAAGTAGGACCTGCCCTGCGC 570
Db 216 rTrpSerThrTrpCysAlaArgThr-----ArgAlaArgThrThrAlaProSerAl 233
QY 571 CAGATGCGCTGGTGGCGCGTTTCTTCTGCGATCGATCTTCGACATCGACACATTGAC 630
Db 233 aProCysThrArgArgThrSerSerGlySerArg----- 245
QY 631 ATCGGCCCCGAGCGCCGCTACTCTGAGCAGAAAGTGGAGCGGTGTGGAGCAGAAC 690
Db 246 -AlaCysProSerAlaAlaThrCysTrp-----ArgTrpAlaAlaThrArgSerArgPr 263
QY 691 ACCCAGGTTGCA---TCCCTACGTGCGGTGGCTGCGCGCCCTACTACTGTGGATT 747
Db 263 oThrSerProArgTrpGlyProTrpCys-----CysProSerProSerSerSerSe 281
QY 748 GGCC---GCTTGGCCAGCGTTGGCCACGCTGACGAGGAGCGGTGGAGCGCGCGCC 804
Db 281 rSerArgAlaCys-----Cys-----SerAlaThrCysSerArgPr 293
QY 805 ATGTTCCCGCCCACTTCTCTGTACAGCAGCTGTGGGAGGACCCCGGCGGATATGAG 864
Db 293 o-----ArgProPro-----ArgArgArgArgProGlnGlyThrProAr 308
QY 865 GTGATGAGATCAACCCCAAGGACACCGTGTGACCTGACTAGCGGCGGTGCAATGCC 924
Db 924 ----- 924
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QY 1451 GCATCCCATTTGAGAACTACATCGCGCCGACCATGAGCGCGCTGGCGGAGAACTCGCAGC 1510
Db 253 ThrAlaPro-----ThrThrAlaSerThrPro-----ArgArgProAlaAlaSer 267
QY 1511 TCGCGAAGCAGAACTACTTCTACTCAACTGCTCACCGGCAAGTTCTCTGCGCGCAAACT 1570
Db 268 SerAlaSerArgThrAlaSerSerSerArgSerProProProThrThrProSerSerAla 287
QY 1571 GCCCACTTACCTGCGCGAGCGGCTTTCGCCACCTCTCAAGAGTGGCGTGGTGGACAACC 1630
Db 288 AlaSerPro-----ArgArgThrArgProProSer----- 297
QY 1631 TGACCGTCTCCACCAACTCTTCTCATGGAGGAGCTCAAGCGCGCACTACACCAAGGTGA 1690
Db 298 -----SerProProThr----- 301
QY 1691 TTCTGATGACCACTGGACTGGCTGGATATGCCCGTGGCCCAACGAGCTGGCGGAGTGCC 1750
Db 302 ----- 304
QY 1751 TGGCCAAAGCAGTTGCGCGGCGCGCATGTCATCTGGCGCTCCGCTCCCTCAGCCCGC 1810
Db 305 ProProSerCysAlaArgProAlaAlaSerSerProGlyThrLeuSerCysSerAlaSer 324
QY 1811 CCTACCGCAGCTGATCC-----AGAAGCGGGCTTCGACGTGCGTGCATCCGCC 1861
Db 325 AlaThrSerSerSerThrSerAlaAlaProSerSerIleCysLeuSerThr 344
QY 1862 GGGCCACTCAGGGCTACATGAGCCGCTCAACATGATCAGACTCTCTTCTACATGGCCCGCC 1921
Db 345 ArgLeuArgArgSerSerLeuArgThrArgMetThrSer----- 358
QY 1922 GGAAGGGCGCCAAAGG 1939
Db 359 -----IleProArgArg 362

RESULT 11
US-11-096-568A-19501
; Sequence 19501, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nickolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; TITLE OF INVENTION: Theory
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 19501
; LENGTH: 544
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(544)
; OTHER INFORMATION: Ceres Seq. ID no. 12373376
US-11-096-568A-19501

Alignment Scores:
Pred. No.: 4, 77e-09 Length: 544
Score: 267.50 Matches: 126
Percent Similarity: 41.6% Conservative: 30
Best Local Similarity: 33.6% Mismatches: 103
Query Match: 7.4% Indels: 116
DB: 11 Gaps: 30

US-10-620-914-44 (1-1947) x US-11-096-568A-19501 (1-544)
QY 205 CGCTCGAACCTCATCTGGTGTGACCTGGTGGT---GGCACTGGGGAGAAATGTCGATATG 261
Db 247 ArgGlyAsnIleLeuSerTyraenLeuGlyHisGly-LeuGlnArg----- 262
QY 262 ATGGCTGATTACATCGACCTGGCGAAGTTCAAGTCCATCTACGTGG---TCGACCTGTGC 318
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Db 263 ----- 275
QY 319 CACTCGCTGTGCGAGTGGCCAAAGGAAGGCGAAGGCTGGAAGTAATGTCACAG 378
Db 275 r-----ArgProAlaAla-----Ar 280
QY 379 GTCTGTGGAGCGCGAGCTTGGCAATTTTCGCCCTGAGGGCACCGCGACGCTCATCACC 438
Db 280 gAlaTrp---ProTrpTrpSerAlaArgPro-----SerProSerArgGlyThrPr 297
QY 439 T-----TCTCTACTCTCCTCAGATGATTCACCGTTCACCAAGCTCATCACCAG 489
Db 297 oGlySerGlyAlaProCysSerSerArg-----ThrProSerSerGlyPr 312
QY 490 GCTTGTCTGTCTCTCT-----CCCAAGACGCG 516
Db 312 oAlaAlaArgArgCysCysProThrGlyAlaAlaThrSerThrAlaProSerThrSe 332
QY 517 CTGG-----TGGCGGTTCGCGACTTTCACGTAGCGGCAAGTACGACCTGCCCTCGCC 570
Db 332 rTrpSerThrTrpCysAlaArgThr-----ArgAlaArgThrThrAlaProSerAl 349
QY 571 CAGATGCCCTGTGCGCGCGTTCCTCTGGCGATCGATCTTCGACATCGACACATTGAC 630
Db 349 aProCysThrArgArgThrSerSerGlySerArg----- 361
QY 631 ATCGCCCGCGCGCGCTCTCTCTGAGCAGAGCTGGAGCGCGTGTGGAGGAGAAC 690
Db 362 -AlaCysProSerAlaAlaThrCysTrp-----ArgTrpAlaAlaThrArgSerArgPr 379
QY 691 ACCCAGGTTTCA---TCCCTACGTGCGGTGGTGGCGGCCCTCTACTAGTGTGGATT 747
Db 379 oThrSerProArgTrpGlyProTrpCys-----CysProSerProSerCysSerSe 397
QY 748 GGCC---GCCTGCGCGAGGTGGCCACGCTGACGAGGAGCGGTGGAGCGCGCGCC 804
Db 397 rSerArgAlaCys-----Cys-----SerAlaThrCysSerArgPr 409
QY 805 ATGTTCCCGCCACCTTCTGTACACGCGAGTCGTGGGAGGACCCCGAGCGCGATATGAG 864
Db 409 o-----ArgProPro-----ArgArgArgArgProProGlnGlyThrProAr 424
QY 865 GTGATGAGATCAACCCCAAGACACCGTGTGTGACCTGTAGCGCGCGCTGCAATGCC 924
Db 424 gProProArgProThrSerArgThr-----SerSerAlaAlaArgSe 437
QY 925 CTGAACCTGTGTGTCAGGGGCGCGCGAGTGTGTGTGGTGGACTGCAACCCCGCGCAG 984
Db 437 rSerThrSerAlaCysThrArgProAlaAlaThrCys----- 449
QY 985 TCGCGCTTCTGAGAGCTGGAAGAGTGGCCATTTCAGCAGCTGGAGTTTGGAGCG--- 1039
Db 450 -----TrpSerThrCysArg-----AlaThrTrpAlaCysAlaThrProTh 463
QY 1040 -----TGTGCGAGCTGTTTCGGGAGGCGGTGACCCCGCATTTGAGAGGTG 1086
Db 463 rTrpArgProProAlaProArgCysThrAlaSerAlaThrProGlnAlaAlaSerGl 483
QY 1087 TACGAGA---AGAAGCTGGCGCCCT---TCTGTGCGAAACCGACCACTTCTGTGTC 1140
Db 483 yThrSerTrpArgThrTrpArgProArgAlaAlaSerAlaAlaThrAlaSerGlySe 503
QY 1141 AAGCGCTCTGTGTACTTCCAGCAGCGCTGTACTTACCAGG-----GGGCGATGGCGAAG 1194
Db 503 rSerProSerGlyArgAlaSerSerAla---ThrAlaArgCysGlyAlaProSerAlaAl 522
QY 1195 CTGTGCTGGTGTGTCAGTGCCTGGCGGTGG---TGCTGGGAC 1234
Db 522 aCysAlaAlaProArgAlaAlaProGlyTrpAspCysValAsp 536

RESULT 12
US-10-131-826A-219
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Best Local Similarity:	23.5%	Mismatches:	223
Query Match:	7.4%	Indels:	118
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 US-10-620-914-44 (1-1947) x US-10-973-115B-319 (1-1076)			
Qy	482	TCGACAGCGTGTCTGCTACTGTCGCCAADAAGCGCCTGGTGCGGTGC CGACTTCTACG	541
Db	216	AlaThrAlaAlaAlaAlaAlaAlaAlaThrAlaThrAlaCysGlyAlaThrThrAlaThrThr	235
Qy	542	TGAGCGCAATACGACCTGCCCTGGCGCAGATGCCCTGGTCGCGCGTTCTTCTCGCC	601
Db	236	AlaAlaAlaAlaAlaGlyAlaAlaAlaAlaCysAlaAlaAlaAlaAlaGly---	254
Qy	602	GATCATCTTCGACATCGACAATTGACATTCGCCCGCGAGCGCGCCTACCTCGSAGC	661
Db	255	-----CysAlaGlyThrThrAlaThrGlyAlaAlaAlaAlaCysThr-----	270
Qy	662	AGAAGCTGGAGCGGTGGGAGCAGAACACCAGGGTTGATCCCCTACGTGCGCGTGC	721
Db	271	-----GlyThrCysAlaAlaThrThrCysAlaAlaGlyAlaAlaCysAlaGly	287
Qy	722	TGSGCGGCC-----CCTACTACGTGGATTGGCGCGCTGCCACGCGTTG	766
Db	288	CysThrThrCysThrGlyThrCysCysThrThrCysThrThrCysAlaThrGlyGlyAla	307
Qy	767	GCCACGCGCTCGACAGAGCGGTGGAGCGCGCCCATGTTCCCGCCACCTTCTCTGT	826
Db	308	AlaGlyAlaCysGlyThrThrThrThrThrGlyGlyThrCysAlaAlaCysThrGlyCys	327
Qy	827	ACAGCAGTCGTGGAGACCCCGAGCGCGATATGGAGGTGATGGAGATCAACCCCAAGG	886
Db	328	AlaAlaThrThrGlyCysAlaAlaGlyGlyCys-----	338
Qy	887	ACAGGTGCTGACCTGACTAGCGCGCTGCATGTCCTGAACCTGCTGTGAGG--	943
Db	339	ThrGlyCys-----AlaAlaGlyAlaAlaAlaAlaThrAlaCysGlyCysThrThr	355
Qy	944	-----GGCGCGCAGGTGCTGCTGGTGACTGTCAAACCCCGCAGTCGGCGC	991
Db	356	ThrGlyThrGlyAlaGlyAlaGlyAlaCysThrThrThrCysAla-----	370
Qy	992	TTCTGGAGCTGAAGAGGTGCCATTGACGAGCTGGAGTTTGAGAGCTGTGGCAGCTGT	1051
Db	371	-----ThralaglyCysCysThrThrAlaGlyGlyCys381	
Qy	1052	TCGCGAGGGGTGCACCGGCATTGAGdAGCTGACGAGAGAGCTGGCGCCCTTCC	1111
Db	382	AlaGlyAlaAlaAlaThrThrGlyAlaGlyCysCys-----Ala394	
Qy	1112	TGTCGCAACACGACCAACTTCTGGTCCAAGCGCCTCTGTACTTCCAGCACGCGCTGT	1171
Db	395	CysThrGlyThrAlaThrThr-----CysCysThrGlyThrGlyCysThrThrCys	412
Qy	1172	ACTACAGGCGCGATGGCGAAGCTGTGCTGG-	1201
Db	413	AlaThrCysAlaGlyCysThrAlaGlyAlaGlyAlaThrGlyAlaAlaAlaThr	432
Qy	1205	TGTCGAGTCGTCGGCGTGTGGAGCTGGGCAAGACCGTCAAGCGCCTCGCCACG	1266
Db	433	CysCysAlaThrThrAlaCysCysAlaGlyGlyAlaThrGlyAlaAlaAlaGlyAla	452
Qy	1265	CGCCCCAATGGAGGACAGCGCGCTGTGGGACAGCAACATGCTCATCCACTTCGTGA	1322
Db	453	AlaThrAlaThrThrThrAlaThrAlaGlyGlyAlaThr-----	466
Qy	1325	AGAACGGGCCAAGCGCTGTGTGGC-----TGTCGTCAAAGT1363	
Db	467	--ThrGlyGlyAlaAlaAlaCysAlaAlaAlaGlyGlyAlaAlaThrCysThrAlaCys	485
Qy	1364	TCGTGACCTGTGTCTTCAACAGCGCGTGTGTGTTCCGGCGGCGGTGCGGGCA	1421
Db	486	AlaAlaAlaGlyCysCysAlaThr-----CysAlaGlyThrGlyAlaAlaCysThrGly	503


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QY 1424 AGCAGTACGCTGATCAAGCGGAGCGCATCCCATTTGAGAACTATACATCGCGGCACCA 1483
Db 504 GlyAla-----ThrAlaThrThrCysThrThrCysThrThrCys 517
QY 1484 TGGACGGCGTGGCGAGAACTCGCAGTCGCGAAGCAAGCACTACTCTTACTACACA----- 1537
Db 518 CysThrGlyGlyAlaThrThrAlaAlaAlaAlaAlaAlaAlaAlaThrThrGlyGly 537
QY 1538 ---ACTGGCTCACCGGCAAGTTCCTGCGCGCAACTGCGCCACCTACCTGCGCGAGGGGG 1594
Db 538 AlaAlaAlaGlyCysAlaGlyThrCysAlaGlyThrAlaAlaAlaAlaCysCysAlaAla 557
QY 1595 CCTTGGCCACCTCAAGAGTCGCTGGTGGCAACCTGACCGTCTCCACCACTTCTTCA 1654
Db 558 GlyCysCysAlaAlaGlyThrAlaCysAlaThrThrGlyAlaThrThrAlaAlaAla 576
QY 1655 TGGAGGAGCTCAAAAGCGCGCACCTACACCAAGTGAATTCGTATGAGACCACCGTGGACTGGC 1714
Db 576 ----- 576
QY 1715 TGGATATCGCGTGGCCAAAGCTGGCGAGTGGCTGGCCAGAGAGTTCGCGGGGCG 1774
Db 577 ---CysAlaGlyThrThrAlaThrThrAlaThrThrGlyAlaAlaAlaAlaThrAlaCysAla 594
QY 1775 GCATCGTCATCGCGCT-----CCGCTCCCTCGAGCCGC 1810
Db 595 AlaThrAlaAlaGlyAlaAlaCysThrGlyCysThrAlaGlyAlaAlaAlaAlaThrAlaThr 614
QY 1811 CCTACGCGAGTGATCAGAGGCGGCTTCGAGCTGCGTGCATCGCGTGCATCGCGCGCCACTC 1870
Db 615 GlyThrThrThrAlaThrAlaAlaCysAlaGlyThrCysThrAlaThrThrCysThr 634
QY 1871 AGGCTACATGACGCGCTCAACATGTACAGCTCCTTCTACA 1912
Db 635 ThrThrThrAlaAlaAlaAlaAlaCysThrThrThrThrThrThr 648

RESULT 14
US-10-137-873A-219
; Sequence 219, Application US/10137873A
; Publication No. US20060084138A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Befesini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Inc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C149
; CURRENT FILING DATE: 2002-04-23
; PRIOR APPLICATION NUMBER: 60/049911
; PRIOR FILING DATE: 1997-06-18
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059117
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; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059122
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059184
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059352
; PRIOR FILING DATE: 1997-09-19
; PRIOR APPLICATION NUMBER: 60/059588
; PRIOR FILING DATE: 1997-09-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 219
; LENGTH: 1076
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-137-873A-219

Alignment Scores:
Pred. No.: 5,53e-09 Length: 1076
Score: 267.00 Matches: 121
Percent Similarity: 33.7% Conservative: 52
Best Local Similarity: 23.5% Mismatches: 223
Query Match: 7.4% Indels: 118
DB: 9 Gaps: 17

US-10-620-914-44 (1-1947) x US-10-137-873A-219 (1-1076)
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QY 482 TCGACCAAGCTTGCTCGTACCTGTCCCAAGACGGCCCTGGTGGCGTTGCCGACTTCTACG 541
Db 216 AlaThrAlaAlaAlaAlaAlaAlaAlaThrAlaThrAlaCysGlyAlaThrThrAlaThrThr 235
QY 542 TGACGGCAAGTAGCAGCTGCCCCCTGCGCCAGATGCCCTGGTGGCGGTTTCTTCTGGC 601
Db 236 AlaAlaAlaAlaAlaAlaGlyAlaAlaAlaAlaCysAlaAlaAlaAlaAlaAlaGly--- 254
QY 602 GATCGATCTTCGACATCGCAACATTCACATCGCCCGCGCGCCCTACCTCGGAGC 661
Db 255 -----CysAlaGlyThrThrAlaThrGlyAlaAlaAlaAlaAlaCysThr----- 270
QY 662 AGAAGCTGGAGCGCGTGTGGGAGCAGAACACCCAGGTTTCGATCCCTACGTGCGGTGGC 721
Db 271 -----GlyThrCysAlaAlaAlaThrThrCysAlaAlaGlyAlaAlaCysAlaGly 287
QY 722 TCGCGGCC-----CCTACTACGTGTGATTGGCGCGCTGCCAGCGTTG 766
Db 288 CysThrThrCysThrGlyThrCysCysThrThrCysThrThrCysAlaThrGlyGlyAla 307
QY 767 GCCACGCCCTGCACGAGGCGCGTGGAGCGCGCCCATGTTCCCGCCACCTTCTCTGT 826
Db 308 AlaGlyAlaCysGlyThrThrThrThrGlyGlyThrCysAlaAlaCysThrGlyCys 327
QY 827 ACAGCAGTCTGGGAGACCCCGAGCCCGGATATGGAGGTGATGGAGATCAACCCCAAGG 886
Db 328 AlaAlaThrThrGlyCysAlaAlaAlaGlyGlyCys----- 338
QY 887 ACAGGTGCTGACCTGACCTAGCGCGCGCTGCATGCTGAACTGCTGGTGCAGG--- 943
Db 339 ThrGlyCys-----AlaAlaGlyAlaAlaAlaAlaThrAlaCysGlyCysThrThr 355
QY 944 -----GGCGCGCGCAGGTGCTGGTGGTGGTGCACCCCGCGCAGTCGGCGC 991
Db 356 ThrGlyThrGlyGlyAlaGlyAlaCysThrThrThrCysAla----- 370
QY 992 TTCTGGAGCTGAAGAAGGTGGCCATTACAGAGCTGGAGTTGAGAGAGCTGTGGAGCTGT 1051
Db 371 -----ThrAlaGlyCysCysCysThrThrAlaGlyGlyCys 381
QY 1052 TCGCGGAGGGCTGCACCCCGCGCATTTGAGGAGCTGTACGAGAAAGCTGGCGCCCTTCC 1111
Db 382 AlaGlyAlaAlaAlaThrThrGlyAlaGlyCysCys-----Ala 394
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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: May 5, 2006, 07:45:05 ; Search time 26 Seconds
(without alignments)
2060.532 Million cell updates/sec

Title: US-10-620-914-45
Perfect score: 3463
Sequence: 1 MGSGRDGPASYTKNFSLE.....RVNMYSSPYMARRKAKKDN 648

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA.*
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2: /cgn2_6/ptodata/1/iaa/6_COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/H_COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	352	10.2	310	2	US-09-248-796A-21233
2	158	4.6	222	2	US-09-248-796A-26335
3	121	3.5	212	2	US-09-107-532A-7254
4	118	3.4	329	2	US-09-902-540-16360
5	111	3.2	195	2	US-09-583-110-4761
6	111	3.2	198	2	US-09-107-433-4622
7	108.5	3.1	706	2	US-09-252-991A-24766
8	107	3.1	255	2	US-09-667-373-2
9	107	3.1	255	2	US-10-305-413-2
10	104.5	3.0	677	2	US-09-489-039A-13088
11	103.5	3.0	1070	2	US-09-107-532A-3716
12	101.5	2.9	663	2	US-09-711-164-332
13	99.5	2.9	471	2	US-08-994-689C-1
14	98.5	2.8	555	2	US-09-134-078-24
15	98.5	2.8	2636	2	US-09-252-991A-25753
16	97.5	2.8	464	2	US-09-134-001C-3488
17	97.5	2.8	471	2	US-08-994-689C-21
18	97	2.8	2209	2	US-10-017-754-1303
19	96.5	2.8	555	2	US-09-252-991A-28313
20	96.5	2.8	2470	2	US-08-265-967C-2
21	96.5	2.8	2470	2	US-08-305-790B-3
22	96	2.8	717	2	US-09-248-796A-18293
23	95.5	2.8	459	2	US-09-949-016-7329
24	94	2.7	480	2	US-09-438-185A-934
25	93.5	2.7	445	2	US-09-252-991A-17629
26	93.5	2.7	471	2	US-09-391-104-25
27	93.5	2.7	475	2	US-09-248-796A-15861

28	93.5	2.7	480	2	US-09-949-016-10560	Sequence 10560, A
29	93.5	2.7	590	2	US-09-489-039A-10743	Sequence 10743, A
30	92	2.7	574	2	US-09-605-703B-254	Sequence 254, App
31	92	2.7	1036	2	US-09-489-039A-10266	Sequence 10266, A
32	91.5	2.6	341	2	US-09-538-092-634	Sequence 634, App
33	91.5	2.6	681	2	US-09-248-796A-16367	Sequence 16367, A
34	91	2.6	749	2	US-10-104-047-2622	Sequence 2622, Ap
35	90.5	2.6	504	1	US-08-645-900A-1	Sequence 1, Appli
36	90.5	2.6	504	1	US-08-882-238A-1	Sequence 1, Appli
37	90.5	2.6	504	1	US-08-667-790A-1	Sequence 1, Appli
38	90.5	2.6	504	2	US-09-220-459-1	Sequence 1, Appli
39	90.5	2.6	504	2	US-08-938-688A-32	Sequence 32, Appl
40	90.5	2.6	504	2	US-08-548-568B-1	Sequence 1, Appli
41	90.5	2.6	504	2	US-08-822-999-3	Sequence 3, Appli
42	90.5	2.6	504	2	US-09-056-285A-8	Sequence 8, Appli
43	90.5	2.6	504	2	US-09-306-828-32	Sequence 32, Appl
44	90.5	2.6	504	2	US-09-952-464A-8	Sequence 8, Appli
45	90	2.6	500	2	US-09-543-681A-6847	Sequence 6847, Ap

ALIGNMENTS

RESULT 1
US-09-248-796A-21233
; Sequence 21233, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 21233
; LENGTH: 310
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-21233

Query Match		10.2%	Score 352;	DB 2;	Length 310;
Best Local Similarity		29.6%	Pred No. 3.1e-30;		
Matches		95;	Conservative 35;	Mismatches 97;	Indels 94; Gaps 8;
QY	144	LITFSYSLTMIPTPPHNVIDQACSYLSQDGLVGVDYFVS	-----GKYD----	LPLRQMP	193
Db	3	LITFSYSLMIPTPPHNVIDQACSYLSQDGLVGVDYFVS	-----GKYD----	LPLRQMP	193
QY	194	WSRFFWRSIFDIDNIDIGPERRAYLEOKLERVNEQNTQ	-----GSIYPVWLRARYVWI	249	
Db	63	WILRFNRFWFEADKFLDSSRRNYLYKFGTVKLSYNKALGKI	-----PYIWI	114	
QY	250	GRLPVGHALHEE-----RVERPPMPFPPT	-----	273	
Db	115	CDKSKSHITILERINCLATESPYLAPTTPTANQLEDIPISKGEAALINQKLPYSM	174		
QY	274	-----FLYTQSMEDPEPDMVMEINPKOTVLTLTSGGCNCL	309		
Db	175	YYQKEYWRVYDENMPLVEQPKQVYIYFTWEDPREDHKLLNFTSDDTVAITSAGDNIL	234		
QY	310	NL--LVQAGQVSVDCNPAQSALLEKKVAIQOLEFEDVWQLFGEGVHPRIEELYEKKL	367		
Db	235	SYASLPTPPKKIHAVDLNPCCQHILLEKLKSLASFCQLSQEQIWSMFGEKGIENFNDLLIDL	294		
QY	368	APFLSQTSHNFWSKRLWYFOH	388		
Db	295	APHMSSNA-----FQH	305		

```
RESULT 2
US-09-248-796A-26335
; Sequence 26335, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstein et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 26335
; LENGTH: 222
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-26335

Query Match          4.6%; Score 158; DB 2; Length 222;
Best Local Similarity 35.1%; Pred. No. 9,7e-09;
Matches 34; Conservative 20; Mismatches 19; Indels 24; Gaps 3;

QY 51 LESFYGPQAAAF-----AARLAERSNLIVDLGGGTGTGVNDMMADYI 92
DB 123 LESFYKNQAHYDNTREFLLKGRQBCRLAISHLPKKDLIWDIGGTGSGNIEMFMDIS 182
QY 93 DLAK-FKSIYVDLCHSLCEVAKKAKA-----KGWK 123
DB 183 KISENFKAVYLDVLSLCEVAKARFESHDLTPRDWK 219

RESULT 3
US-09-107-532A-7254
; Sequence 7254, Application US/09107532A
; Patent No. 6583275
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; NUMBER OF SEQUENCES: 7310
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-ROM ISO9660
; COMPUTER: PC
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,532A
; FILING DATE: 30-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/085,598
; FILING DATE: 14 May 1998
; APPLICATION NUMBER: 60/051571
; FILING DATE: July 2, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ariniello, Pamela Deneke
; REGISTRATION NUMBER: 40,489
; REFERENCE/DOCKET NUMBER: GTC-012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781)893-5007
; TELEFAX: (781)893-8277
; INFORMATION FOR SEQ ID NO: 7254:
```

```
;
;
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 212 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein
;   HYPOTHETICAL: YES
;   ORIGINAL SOURCE:
;   ORGANISM: Enterococcus faecium
;   FEATURE:
;     NAME/KEY: misc feature
;     LOCATION: (B) LOCATION 1...212
;   SEQUENCE DESCRIPTION: SEQ ID NO: 7254:
US-09-107-532A-7254

Query Match          3.5%; Score 121; DB 2; Length 212;
Best Local Similarity 30.6%; Pred. No. 0.00013;
Matches 33; Conservative 23; Mismatches 44; Indels 8; Gaps 3;

QY 73 IWDVLGGGTGVNDMMADYIDLAKFKSIYVVDLCHSLCEVAKKAKAGWKNVQVVEADA 132
DB 53 VLDYGGGTGLVSLPLAE-----RFKELIIADASETMLKMAEEKIQADLKNVRTIHADA 107
QY 133 -CFAPPEGTATLITFSYSLTMIPPHNVIDQACSYLSQDGLGVGVADF 179
DB 108 SVER--PAVQANLILLSLVLLHIPOTENILTKLYEILLAPGGQLIIVDF 153

RESULT 4
US-09-902-540-16360
; Sequence 16360, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 16360
; LENGTH: 329
; TYPE: PRT
; ORGANISM: Myxococcus xanthus
US-09-902-540-16360

Query Match          3.4%; Score 118; DB 2; Length 329;
Best Local Similarity 21.8%; Pred. No. 0.00059;
Matches 81; Conservative 37; Mismatches 121; Indels 132; Gaps 16;

QY 264 VERPPMFPPTFLYTSQSWEDPEPMVMEINPKDVTLTSGGCNALLNLVQ-GAGQVVSV 322
DB 6 VSTPEL---RLKFAVREDAALELALVERTRARAVLTVASGGCTLLTLARRHPALELVGF 62
QY 323 DCNPAQSALLELKKVAIQQL-----EPEDVWQLFG-----EGVHPRIEELYEKKLAPFL 371
DB 63 DFNPRQLAHVREKAEGLRPLARYSDAEDAAALNQRGEFGLFRTLRRFIEEFVAP-- 120
QY 372 SQTSHNFSKELWYFQHGLYYQGGMGKLCWLQCLAVVLGLGKTVKRLANAP-TMEEORR 430
DB 121 ---AHE-----LAFF-----APATTASORR 138
QY 431 LWDSNMLIHFKVNGPKPLVWLFVKFVSLVLFNKAVLWFGGVPKGQYALIKADGIPIENY 490
DB 139 -----EACARWFA--PYWPVAFELAAAPLEN- 164
QY 491 IARTMDGVAENSHVRKQNY-----FYNCLTKGFLRDNCTYLR 529
DB 165 ---TMFGPAATQHAEPGSGYPGYFOAVFERGLQREDAPRNPFLQHVLLGRYLRDAPAYLR 221
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; SEQ ID NO 13088
; LENGTH: 677
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-13088

Query Match
Best Local Similarity 3.0%; Score 104.5; DB 2; Length 677;
Matches 63; Conservative 29; Mismatches 91; Indels 111; Gaps 15;

235 IPYVWLRAPYVWIGRLPSVGHALH-----EERVERPPMP-PFELYTQSWEDPE 284
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
193 IEYSPGVGVVDYWIWALQSGITLTGTINFFVTIIMRAPGTMFMPVF-----SWASLC 248
QY | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
285 PDMEVMEINPKDVTILTLTSGGCNALLVQAGQVVSVCNPAQSAALLEKKVAIQLEF 344
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
249 ANILIIASFP--ILTVT-----JALLTLDRYLGTHTFT 279
QY | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
345 ED-----VWQLFGEVHPRIELEYEKKLAPP--LSQTSINFWSKRLWYFQHG 391
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
280 NDMGGMNMYINLIW-AWG---HP---EYILVLPVFGVFSIAATFSRKRLF----- 325
QY | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
392 YQGGMGKLCWLQCLAV-----LGLGKTVKRLANAPTMEQORRLWDSNMLIHF 440
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
326 ---GVTSLWATVCITVLVSFVILWHLHPTMGAGANNVAFGITT-----IIA 370
QY | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
441 VKNGPKPLVWLFVKFVSLVFNKAVLW-----FGG-----GVPGKOVAL 479
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
371 IPTGVKIFNWLFTYQGRIVFNSAMMTIGFIVTFSVGMTGVLLAVPGADFVL 424

RESULT 11
US-09-107-532A-3716
; Sequence 3716, Application US/09107532A
; Patent No. 6583275
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 7310
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-ROM ISO9660
; COMPUTER: PC
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,532A
; FILING DATE: 30-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/085,598
; FILING DATE: 14 May 1998
; APPLICATION NUMBER: 60/051571
; FILING DATE: July 2, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ariniello, Pamela Deneka
; REGISTRATION NUMBER: 40,489
; REFERENCE/DOCKET NUMBER: GTC-012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781)893-5007
; TELEFAX: (781)893-8277
; INFORMATION FOR SEQ ID NO: 3716:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1070 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
```

```
; HYPOTHETICAL: YES
; ORIGINAL SOURCE:
; ORGANISM: Enterococcus faecium
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (B) LOCATION 1....1070
; SEQUENCE DESCRIPTION: SEQ ID NO: 3716:
US-09-107-532A-3716

Query Match
Best Local Similarity 3.0%; Score 103.5; DB 2; Length 1070;
Matches 80; Conservative 54; Mismatches 113; Indels 113; Gaps 18;

260 HEERVERPPMPPTFLYTQSWEDPEPDMEVMEINPKDVTILTLTSGGCNALLVQGA--- 316
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
491 HQPKIE-----VTETGSLDIRFOVTGIEQEIDHVLQ-----SLLRNDAPVT 533
QY | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
317 ---GVVSVDCNPAQ--SALLELEKVAIQ-----OLE-----FEDVW 348
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
534 LENGQVLSFDSEEFQOTSQVILQQLRESIRTEGTHVPKNQGLIIFQLEKSNATFSSEF 593
QY | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
349 Q-LFCEGVHPRIELEYEKKLAPFLSQTSHNF-----WSKELWYFQHGLYQGGMGKLCW 401
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
594 QTMVQDLIHP---ERYQQLPKGLNATWRDYKQGFRLMKMLCHYQFG----- 638
QY | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
402 VLQCLAVVLGLGKTVKRLANAPTMBEQORRLWDSNMLIHFNKNGPKPLVW-----LFVK 454
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
639 --GILADEMGLGKTLQTTIAFLSEKERKSFSAIV-----APASLIYNWQAEVRKFPAP 690
QY | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
455 FVSLVFNKAVLWFGGVPQKQYALIKADGPIENYIARTMDGVAENSHVRKQNYFYNC 514
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
691 SLSTQVIN-----GNKKEREELLAKOTDIRVTSYASLRQD--LANYQSQKIDYL---I 738
QY | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
515 LTGRFLRDNCP-----VLRERAA-----PATLKSQVVDNL-----TVSTNPFMEELKAR 558
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
739 LDEAQMVKNSTKTAQALRELAVPQRFALSGTPIENNLEELWSLFPATIMPGFPTKTKR 798

RESULT 12
US-09-711-164-332
; Sequence 332, Application US/09711164
; Patent No. 6589738
; GENERAL INFORMATION:
; APPLICANT: Forsyth, R. Allyn
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; TITLE OF INVENTION: GENES ESSENTIAL FOR MICROBIAL PROLIFERATION AND ANTISENSE THERET
; FILE REFERENCE: ELITRA.008A
; CURRENT APPLICATION NUMBER: US/09/711,164
; CURRENT FILING DATE: 2000-11-09
; PRIOR APPLICATION NUMBER: US 60/164415
; PRIOR FILING DATE: 1999-11-9
; NUMBER OF SEQ ID NOS: 469
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 332
; LENGTH: 663
; TYPE: PRT
; ORGANISM: Escherichia coli
US-09-711-164-332

Query Match
Best Local Similarity 2.9%; Score 101.5; DB 2; Length 663;
Matches 63; Conservative 35; Mismatches 95; Indels 91; Gaps 15;

235 IPYVWLRAPYVWIGRLPSVGHALHEERVERPPMPPTFLYTQSWEDPEPDMEVMEINP 294
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
179 IEYSPGVGVVDYWIWLSQLSGIGTTLTGIN-----FFVTILMKRA-----PGMTMFKM-P 226
QY | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
295 KDTVLTLTSGGCNALLVQAGQVVSVCNPAQSAALLEKKVAIQLEFED----- 346
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
227 VFTWASLCA-----NVLIINASFFILITVV-----ALLTLDRYLGTHTFTNDMGNNMY 275
QY | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
347 ---VWQLFGEVHPRIELEYEKKLAPP--LSQTSNFWSKRLWYFQHGLYQGGMGKLCW 401
```

Db 276 INLIW-ANG---HP---EVYIILFPVGFVSEIAATFSKRLF-----GYTSLVM 318
QY 402 VLQCLAVV-----LGLGKTVKRLANAPTMEEORRLWDSNMLIHFKVNGPKPLVW 450
Db 319 ATVCITVLSFIVLWHLHFFTMGAGANVNAFFGITTM-----IIAIPYGVKIFNW 366
QY 451 LFKVKSIVSLVFNKAVLW-----FGG-----GVPGKQVAL 479
Db 367 LFTMTQGRIVFHSAMLWTGIFVTVSGVGMTVLLAVPGADFVL 410

RESULT 13

US-08-994-689C-1
; Sequence 1, Application US/08994689C
; Patent No. 6613958
; GENERAL INFORMATION:
; APPLICANT: Neuhold, Lisa
; APPLICANT: Killar, Lotan
; TITLE OF INVENTION: TRANSGENIC ANIMAL MODEL FOR
; TITLE OF INVENTION: DEGENERATIVE DISEASES OF CARTILAGE

; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESS: Darby & Darby PC
; STREET: 805 Third Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10022

COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/994,689C

; FILING DATE: 1997-12-19
; CLASSIFICATION: 800
; PRIOR APPLICATION NUMBER:
; APPLICATION NUMBER:
; FILING DATE:

ATTORNEY/AGENT INFORMATION:
; NAME: Grean, Reza
; REGISTRATION NUMBER: 38,475
; REFERENCE/DOCKET NUMBER: 0630/0D532
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-527-7700
; TELEFAX: 212-753-6237
; TELEX: 236687

INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 471 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-994-689C-1

Query Match 2.9%; Score 99.5; DB 2; Length 471;

Best Local Similarity 18.4%; Pred. No. 0.13;

Matches 100; Conservative 61; Mismatches 159; Indels 223; Gaps 27;

QY 51 LESFVGP-----QAAFAAALRAERSNLIWDLGGGTGEN-VDNM-----ADYIDLA 95
Db 43 LRSYHPTNLALGILKENAASSMTERLRMSQSFGLVETGKDDNTLDVNMKPRCGVVDVG 102
QY 96 KFKSI-----YVVDLCHSLCEVAKKAKGKNVQVVEADACQFAPP 138
Db 103 EYNVFPRLKWSKMLTYRIVNYTFDMTHSEVEKAFKA-FKVMSDVTPLN-----152
QY 139 EGTATLITFSYSLTWIPPHNVIDQACSVLSODGLVGVDIFY-VSGKYDLPURQMPWRR 197
Db 153 -----FTRLHDGIADIMISFGIKEHGDFYFPDGPGLLAHAFPPGFN 194

QY 198 FFWRSIPDIDNIDIGPERRAYLEQKLERVWEQNTQGSIPYVPMRLRAPYVYVWIGRLPSVGH 257
Db 195 YGGAHFDHDD-----ETWTSKSG-----YNLFVAHAHEFGH 226
QY 258 ALHEERVERPP--MPPPTFLYTQSWDEPPDMEVMEI-----NPKDVTVLTLTSG 304
Db 227 SGLDHSKDPGALMF-PIYTYTGKSHFMLPDDDVQGIQSLYXPGGDEDPNPKH-----277
QY 305 GCNALNLLVQAGAGVSVDCNPAQS--ALLKKVAIOOLEFED--VMQLFGEVGHVHP---357
Db 278 -----PKTPDKCDPSLSLDAITSLRG---ETMIFKORFFWRL-----HPOOV 316
QY 358 -----RIEELYEKKLAPFLSOTSHNFWSKRLWYFOHGLYXQGGMGKLCW 401
Db 317 DAELFLTKSWFPELPNRIDAAYE-----HPSHDL-----IFIPR-----GRKEW 355
QY 402 VLQCLAVV-----LGLGKTVKRLANAPTMEEORRLWDSNMLIHFKVNGPKPLVWLF 452
Db 356 ALNGVDILLEGYPKKISLGLPKVKKISAA-----VHPEDTG-----392
QY 453 VKFVSLVLPNKAVLW---FGGVFGKQYALIKADGIPNIENYIARTMDGVAENSHVKQNY 509
Db 393 ----KTLFSGNQVMRYDDTNHIMDKOYPRLIEEDFP---GIGDKVDAYE-----KNGY 440
QY 510 FYY 512
Db 441 IYF 443

RESULT 14

US-09-134-078-24
; Sequence 24, Application US/09134078
; Patent No. 6368844
; GENERAL INFORMATION:
; APPLICANT: Bylina, Edward J.
; TITLE OF INVENTION: GLYCOSIDASE ENZYMES
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Gray Cary Ware & Freidenrich LLP
; STREET: 4365 Executive Drive, Suite 1600
; CITY: San Diego
; STATE: CA
; COUNTRY: USA
; ZIP: 92121
COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/134,078
; FILING DATE: 13-AUG-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/949,026
; FILING DATE: 10-OCT-1997
; APPLICATION NUMBER: 60/056,916
; FILING DATE: 06-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Haile, Lisa A.
; REGISTRATION NUMBER: 38,347
; REFERENCE/DOCKET NUMBER: 09010/024002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 858/677-1456
; TELEFAX: 858/677-1465
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 555 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal

US-09-134-078-24

Query Match 2.8%; Score 98.5; DB 2; Length 555;
Best Local Similarity 18.9%; Pred. No. 0.23;
Matches 111; Conservative 74; Mismatches 166; Indels 23

111	Qy	111	EVAKKAKAK-----GWKNVQVVEADACQAPPEGTATLITSYSLTMTIPPHNVID- 162
50	Db	50	EVLRTKAPEKVLNNQSWGPCRV--DAFSKDPEDP--NWRYSASVVP--DVLIR 101
163	Qy	163	--QACSVLSDGLV-GVADFVVSQKDYDLPLRQMPWSRRFFWRSIFEDIDNIDIGP-ERRAY 218
102	Db	102	NLQSDYFVAEEGKYG---FLSSKIAHPFAVEDGELVAYLEYFDFVEFDFVLEPLV 157
219	Qy	219	LEOKLRVMEQNTQGSIPYYPWLRAPYYVWIGRLPSVGHALHEERVRPMPFPT----- 273
158	Db	158	LED-----PNTPLLEKXAEVLGM-----ENNAARVPKHTGTGWCWS 193
274	Qy	274	--FLYQTSWBDDPDM-----EVMENPK-----DVLTLTSGGCNALNLVQAG 317
194	Db	194	YHYFLDITWETLKNLKLAKNFPPEVQIDDAYEKKDGMVL-----RG 238
318	Qy	318	QVVSVDCNPAQSALLELKVAIQOLEBEDVW-----QLRGEGVHPR--IEELYEK 365
239	Db	239	DFPSVE-----ENAKVIAENGFIPIGWAPTAFPSVSETSDVENE--HPDWVVKENGEP 287
366	Qy	366	KLAPFLSQTSHNFWSKRLWYFQHGLYYQGGMGKLCWLQCLAVVLGLKTVKRLANAPTM 425
288	Db	288	KWA-----YRNWNKKIY-----ALDLSK----- 305
426	Qy	426	EBQRLWDSNMLIHFVXNGPKPLVWLFKVFSVL-----VLFNKAVLWFGGVGVPQKQYALIK 481
306	Db	306	-----DEVLNWLPDSSLRKMGRYRPFKIDFLFAGAVPGER---K 342
482	Qy	482	ADGIPNIY---IARTMDGVAENS-----HVRKQ 507
343	Db	343	KNITPQAFKKGITETRKAVGEDSFILGCGSPLLPAVGCDWGRIGPDPTAPFWEHIEDN 402
508	Qy	508	-----NYFYNCITGKFLRD-----NCPTYL-----REAAAFATLKSGVVNDLTVS 547
403	Db	403	GAPAAERWALENAITRYFMDHDFWLNDPCLILREKTDLTQKEKELYSYTCVGLDNMIIE 462
548	Qy	548	TNPFMBELK-ARTVTKVILMDHVDWLD--MPVANELAECLAKQVAPGG 592
463	Db	463	S-----DDLVLVRDHGKKVLKETLELLGCRPRVQNMISDLRYETVSSG 506

RESULT 15

RESOLUTION 13
US-09-252-991A-25753
: Sequence 25753. Application US/09252991A

```

; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 25753
; LENGTH: 2636
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-25753

```

Query Match 2.8%; Score 98.5; DB 2; Length 2636;
Best Local Similarity 20.6%; Pred. No. 3.4;
Matches 124; Conservative 68; Mismatches 231; Indels 179

127	Qy	VVEDACQFAPPEGTATLIITSYSLTWIPPHNVIDQACSYLSDQGLGVADFFYVSGKYD 188
379	Db	VLGAQAQDLDLFFERLVEAFKVERSLSHSPFLQVVMYNHQPLVADIEALDSVA-----G 430
187	Qy	LPLRQMPWSRRFFWRSIFD--IDNIDIGPERRAYLE-----OKLERVWE----- 228
431	Db	LSFGQLDWGR---TTQFDLSLDIYKGGRLYALTYATDIFEARTVERMARHQNLLRG 487
229	Qy	--QNTQSGIPIYVPWLRAP--YYVWIG-----RLPSVGHALHEERVERPMPPTFLY 276
488	Db	MLENPOASVDSLPLMDABERYOLLEGWNATAAEYPLQGVHRLPEEQVERTPTAPALAF- 546
277	Qy	TQSWEDDEPDMEVMEINPKOTVL--TLTSGGCN-----ALNLLVOGAG 317
547	Db	-----GEERLDYAEENRRNRLAHALIERGVGADRLGVAMERSIEMVVALMALKAGG 600
318	Qy	QVVSVDGN-PAQSALLEKKVAIOQLPEPDMVQL-FGEGVH-----PRIEELYEKKL 367
601	Db	AYVPVDPEYPERQAYMLEDGVLLSQSOSHLKPLAQGVQIRDLDRGAPWEDYSEAN- 659
368	Qy	APFLSQTSHNFWSKRLWYFOHGLYYOQGMGK-----LCWVLOCLAVVLGLG 413
660	Db	-PDIHLGDN-----LAYVIYTSGSTGPKGAGNRHSALSNNRLCWMOQ--AYGLGVG 708
414	Qy	KTVKRLANAPTEBQRRLWDSNNMLIHFYKNGPKPLVMLFVKFVSLVLFNKAVLWFGGG-- 471
709	Db	DTV-----LQKTPSFDVS-----VWEF--FWPLMSGARLVVAAPGDHR 745
472	Qy	VPGQYALIKADGIPENYIARTMDGVAENSHVRKQNYFFYNCLTGKFLRDNCPYLREA 531
746	Db	DPAKLVELINREGVDTLHFVPSMLQAFLODEDAVASTSLKRIVCSEAL-----PADAQOQ 801
532	Qy	APATLKSQVDNLTVSNFFMEELKARTYTKVILMDHVDWLDM-----PVANEL 580
802	Db	VFAKLPOAGLYNLGYPTE-----AAIDVTHMTCEEGKDAVPIGRPIAN-- 845
581	Qy	AECLAKQVAPGGIWIWRSASLSP--PYAEL--IQKAGFDVRCIRRATQGVMDRVNNMYSFY 637
846	Db	----LACYILDG-----NLEFPVPGVLGELYLAG-----RGLARGYHQRPGLTAERF 888
638	Qy	MA 639
889	Db	VA 890

Search completed: May 5, 2006, 07:46:28
Job time : 28 secs

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: May 5, 2006, 07:48:33 ; Search time 87 Seconds
(without alignments)
3112.108 Million cell updates/sec

Title: US-10-620-914-45

Perfect score: 3463

Sequence: 1 MGSGRDGRPASYYTKNFSLE.....RVNYSFYMARRKAKKDN 648

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA_Main:

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
- 6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3463	100.0	648	US-10-620-914-45	Sequence 45, Appl
2	891	25.7	752	US-10-741-849-7021	Sequence 7021, Ap
3	850.5	24.6	908	US-10-620-914-50	Sequence 50, Appl
4	379.5	11.0	416	US-10-118-495-3	Sequence 3, Appli
5	379.5	11.0	416	US-10-620-914-3	Sequence 3, Appli
6	326.5	9.4	416	US-10-118-495-29	Sequence 29, Appl
7	326.5	9.4	416	US-10-620-914-29	Sequence 29, Appl
8	321	9.3	415	US-10-118-495-41	Sequence 41, Appl
9	321	9.3	415	US-10-620-914-41	Sequence 41, Appl
10	292.5	8.4	416	US-10-118-495-33	Sequence 33, Appl
11	292.5	8.4	416	US-10-620-914-33	Sequence 33, Appl
12	123	3.6	2284	US-10-684-141-58	Sequence 58, Appl
13	123	3.6	2284	US-10-810-486-58	Sequence 58, Appl
14	120	3.5	221	US-10-118-495-35	Sequence 35, Appl
15	120	3.5	221	US-10-620-914-35	Sequence 35, Appl
16	119	3.4	2286	US-10-684-141-54	Sequence 54, Appl
17	119	3.4	2286	US-10-810-486-54	Sequence 54, Appl
18	112.5	3.2	672	US-10-282-122A-68178	Sequence 68178, A
19	111	3.2	198	US-10-617-320-4622	Sequence 4622, Ap
20	110.5	3.2	298	US-10-450-783-38334	Sequence 38334, A
21	107	3.1	255	US-10-220-381-24	Sequence 24, Appl
22	107	3.1	255	US-10-988-984-2	Sequence 2, Appli
23	107	3.1	691	US-10-732-923-9665	Sequence 9665, Ap
24	106.5	3.1	670	US-10-282-122A-69771	Sequence 69771, A
25	106	3.1	472	US-09-974-238-120	Sequence 120, App
26	106	3.1	472	US-10-247-671-186	Sequence 186, App
27	106	3.1	472	US-10-211-462-201	Sequence 201, App

28	106	3.1	472	4	US-10-468-406-2	Sequence 2, Appli
29	106	3.1	472	5	US-10-370-715B-256	Sequence 256, App
30	106	3.1	852	4	US-10-437-963-108559	Sequence 108559,
31	106	3.1	2039	4	US-10-369-493-21994	Sequence 21994, A
32	104.5	3.0	663	4	US-10-282-122A-59897	Sequence 59897, A
33	104.5	3.0	664	4	US-10-389-647-469	Sequence 469, App
34	104	3.0	225	4	US-10-118-495-42	Sequence 42, Appl
35	104	3.0	225	4	US-10-620-914-42	Sequence 42, Appl
36	103.5	3.0	1064	5	US-10-732-923-8191	Sequence 8191, Ap
37	103	3.0	908	4	US-10-437-963-132823	Sequence 132823,
38	101.5	2.9	663	3	US-09-815-242-10070	Sequence 10070, A
39	101.5	2.9	663	4	US-10-287-274-332	Sequence 332, App
40	101.5	2.9	663	4	US-10-282-122A-56452	Sequence 56452, A
41	101	2.9	652	4	US-10-282-122A-73132	Sequence 73132, A
42	101	2.9	679	4	US-10-282-122A-48489	Sequence 48489, A
43	100	2.9	323	4	US-10-437-963-162897	Sequence 162897,
44	99.5	2.9	471	4	US-10-375-884-1	Sequence 1, Appli
45	99.5	2.9	663	3	US-09-815-242-14080	Sequence 14080, A

ALIGNMENTS

RESULT 1

US-10-620-914-45
; Sequence 45, Application US/10620914
; Publication No. US20040093639A1
; GENERAL INFORMATION:
; APPLICANT: Benning, Christoph
; APPLICANT: Riekhof, Wayne
; TITLE OF INVENTION: Compositions and Methods for the Production of Betaine Lipids
; FILE REFERENCE: MSU-07769
; CURRENT APPLICATION NUMBER: US/10/620,914
; CURRENT FILING DATE: 2003-07-16
; PRIOR APPLICATION NUMBER: 10/118,495
; PRIOR FILING DATE: 2002-04-08
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 45
; LENGTH: 648
; TYPE: PRT
; ORGANISM: Chlamydomonas reinhardtii
US-10-620-914-45

Query Match 100.0%; Score 3463; DB 4; Length 648;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 648; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MGSGRDGRPASYYTKNFSLEKLLSSMKDDLTVLRLHMMFGSKGDDHAARLESFYGPQAA	60
Db	1	MGSGRDGRPASYYTKNFSLEKLLSSMKDDLTVLRLHMMFGSKGDDHAARLESFYGPQAA	60
Qy	61	APFAARLAERSNLIWVDLGGGTGENVDMADYIDIAKFKSIYVDLCHSLCEVAKKAKAK	120
Db	61	APFAARLAERSNLIWVDLGGGTGENVDMADYIDIAKFKSIYVDLCHSLCEVAKKAKAK	120
Qy	121	GWKNQVQVEADACQAPPEGTATLITFSYGLTMIPPPHNVIDQACSYLSQDLGVADVY	180
Db	121	GWKNQVQVEADACQAPPEGTATLITFSYGLTMIPPPHNVIDQACSYLSQDLGVADVY	180
Qy	181	VSGKYDLPLRQMPNSRRFFWRSIFDINDIDIGPERRAYLEQKLRVWEQNTQGSIPYVPW	240
Db	181	VSGKYDLPLRQMPNSRRFFWRSIFDINDIDIGPERRAYLEQKLRVWEQNTQGSIPYVPW	240
Qy	241	LRAPYYWIGRLPSVGHALHEERVERPMPPTFLYTQSWEDPEDPMEVMEINPKDTVLT	300
Db	241	LRAPYYWIGRLPSVGHALHEERVERPMPPTFLYTQSWEDPEDPMEVMEINPKDTVLT	300
Qy	301	LTSGCCNALNLLVQAGQVSVDCNPQASALLEKKVAIQOLEFEDVWQLFEGVHPRIE	360
Db	301	LTSGCCNALNLLVQAGQVSVDCNPQASALLEKKVAIQOLEFEDVWQLFEGVHPRIE	360

QY 361 ELYEKKLAPLPSOTSHTNFWSKLWYFQHGLYQGGMGKLCWVLOCLAVVLGKTVKRLA 420
DB 361 ELYEKKLAPLPSOTSHTNFWSKLWYFQHGLYQGGMGKLCWVLOCLAVVLGKTVKRLA 420
QY 421 NAPTMEQRRLWDSNMLIHFKVNGPKPLVWLFVKFVSLVLFNKAIVLWFGGVPKGQYALI 480
DB 421 NAPTMEQRRLWDSNMLIHFKVNGPKPLVWLFVKFVSLVLFNKAIVLWFGGVPKGQYALI 480
QY 481 KADGPIENYARTMDGVAENSHVRKQNYFYNYNCLTGKFLRDNCTYLRBAAPATLKSGV 540
DB 481 KADGPIENYARTMDGVAENSHVRKQNYFYNYNCLTGKFLRDNCTYLRBAAPATLKSGV 540
QY 541 VDNLTVSNFMEELKARTYTKVILMDHVDMLDMPVANELAECLAKQVAPGGIIVRSAS 600
DB 541 VDNLTVSNFMEELKARTYTKVILMDHVDMLDMPVANELAECLAKQVAPGGIIVRSAS 600
QY 601 LSPPYAELIQAGFDVRCIRRATQGYMDRVNMYSSFYMARRRGAKKON 648
DB 601 LSPPYAELIQAGFDVRCIRRATQGYMDRVNMYSSFYMARRRGAKKON 648
RESULT 2
US-10-741-849-7021
; Sequence 7021, Application US/10741849
; Publication No. US20050019931A1
; GENERAL INFORMATION:
; APPLICANT: Roemer, Terry
; APPLICANT: Jiang, Bo
; APPLICANT: Boone, Charles
; APPLICANT: Busey, Howard
; TITLE OF INVENTION: Nucleic Acids Encoding Anti-fungal Drug Targets and Methods of
; TITLE OF INVENTION: Use
; FILE REFERENCE: 10182-023-999
; CURRENT APPLICATION NUMBER: US/10/741,849
; CURRENT FILING DATE: 2003-12-19
; PRIOR APPLICATION NUMBER: US 60/434,832
; PRIOR FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 8000
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 7021
; LENGTH: 752
; TYPE: PRT
; ORGANISM: Candida albicans
US-10-741-849-7021

Query Match 25.7%; Score 891; DB 5; Length 752;
Best Local Similarity 32.7%; Pred. No. 4.4e-80;
Matches 229; Conservative 98; Mismatches 232; Indels 142; Gaps 21;

QY 51 LESFYGPQAAAF-----AARLAERSNLIWDLGGGTGENVDMADYI 92
DB 70 LESFYKNOAHYDNTREFLLKGRQECRLRAISHLPKKKDLIWDIGGGTGSNIEPMDIS 129
QY 93 DLAK-FKSIYVVDLCHSLCEVAKKAKAGKQNVQVVEADACQAPPBGTATLITFSYSL 151
DB 130 KISENFKAVYLVDSLPSLCEVAKARFEAHETNVHVLVADACDFIIDYDSADLITFSYSL 189
QY 152 TWIPPFHNVIDOACSYLSQDGLGVADFYVS-----GKYD-----LPLRQMPWSRRFPWR 201
DB 190 SMIPTFNAIDNAVSKLDMEGIIATVDFGIQSSDTSMGRIINTVGLVNRDIPWILRNFWR 249
QY 202 SIFDIDNIDIGERRAYLEQKLERWEQNTQ-----GSIPYVPLWLRAPYVVMIGRLPSVGH 257
DB 250 IWFEDAKVFLDSSRRNILEYKFGTVKLSNYSNKA LGKI-----PYIWIIGCDKSKSH 301
QY 258 ALHEE-----RVERPMPFPPT-----PIANQLEDIPISKHEAALINLQKLPYPSMYQKEYR 361
DB 302 TILERLNCIATESPIATPTPIANQLEDIPISKHEAALINLQKLPYPSMYQKEYR 361
QY 274 -----FLYTSQWEDPEPDMVEINPKDVTLTLSGGCNALNL--LVQG 315
DB 362 VYDEMNPYBQFNQYIYAFTWEDPREDHKLNFTSDDTVLTAITSAGDNILSVASLPTP 421

QY 316 AGQVSVDCNPAQSALLLEKKVAIQOLEFFEDWOLFEGGVHPRIBELYEKKLAPLSOTS 375
DB 422 PKKIHADVNLPCQHLLLELKLASFRCIJSQEQIWSMFGECKTENFNDLLIDTLAPHMSNA 481
QY 376 HNFWSKR--LWYFQHGLYQGGMGKLCWVLOC---LAVVLGKTVKRLANAPTMEEQRR 430
DB 482 FOYWNMDKGPKTFSKGGLY--DTGFSRWALRLSRVYFKVCGVS KYVEELCAATTMEEQRL 538
QY 431 LWDNMLIHFKVNGPKPLVWLFVKFV-SLVLFNKAIVLWFGGVPKGQYALIKADGIPLEN 489
DB 539 IWEHLL-----KPT--LFPNVPVGLSLVGNPMFLWKALGVSPANQAALM---GPSVIK 584
QY 490 YIARTMDGVAENSHVRKQNYFYNYNCLTGKFLRDNCTYLRBAAPATLK-----SGVV 541
DB 585 YVDTLDPIIKRSMISNDNRYFYLCMGRYTKNCPDYLTGKFNRLSSTAATAGSSSPI 644
QY 542 DNLTVSTNPFME---ELKARTYTKVILMDHVDMLD---MPVANELAECLAKQVAPGGIIV 595
DB 645 DNLRIHTDLNEVFGRLKEKSITTAIIMDHMDWDFDPNGRDAINEIT-ALKRCLAPGGRVL 703
QY 596 WRSASLSPPYAEILQKAGF-DVRCIRRATQGYMDRVNMYSS 635
DB 704 LRSASTKFWYLKTFKNLGFQEEENVVRQPGSSIDRVNMYAN 744
RESULT 3
US-10-620-914-50
; Sequence 50, Application US/10620914
; Publication No. US20040093639A1
; GENERAL INFORMATION:
; APPLICANT: Benning, Christoph
; APPLICANT: Riekhof, Wayne
; APPLICANT: Klug, Rouven
; TITLE OF INVENTION: Compositions and Methods for the Production of Betaine Lipids
; FILE REFERENCE: MSU-07769
; CURRENT APPLICATION NUMBER: US/10/620,914
; CURRENT FILING DATE: 2003-07-16
; PRIOR APPLICATION NUMBER: 10/118,495
; PRIOR FILING DATE: 2002-04-08
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 50
; LENGTH: 908
; TYPE: PRT
; ORGANISM: Neurospora crassa
US-10-620-914-50

Query Match 24.6%; Score 850.5; DB 4; Length 908;
Best Local Similarity 30.4%; Pred. No. 7.3e-76;
Matches 222; Conservative 105; Mismatches 235; Indels 169; Gaps 18;

QY 69 RSNLIWDLGGGTGENVDMADYIDLAK-FKSIYVVDLCHSLCEVAKKAKAGKQNVQV 127
DB 178 RRKPIWVDVGGGTGNIEAMAKFVNVSFFKTVYLVDFSPSLCEVARKRFARLGWENVRV 237
QY 128 VEADACQFA-----PPEGT-----ATLITFSYSLTWIPPF 157
DB 238 ICTDARKFRLDYEDVDEGESGSDSPSLSGWGETKPGRHAGAEILITMSYLSLMDPY 297
QY 158 HNVIDOQACSYLSQDGLGVADFYVSGKYD-----LPLRQMPWSRRFPWRISIFDIDN 208
DB 298 FSIIDSLESLLAPHGLIAVDFYAQSKVDFTFRNYTGGLMNRHVGYFARNEWRWSFDADR 357
QY 209 IDIGERRAYLEQKLERW-----FQNTQGSIPYVPW---LRAPYV----- 247
DB 358 VSLPARRDYLEFRGTVLTVNARNNTLGAIPYIWLGLCKLPKPFSTSLPHEIVSHIDAI 417
QY 248 -----WIGR-----LPSVGHALH 260
DB 418 ATESPRSSRLVGKSSSATNALAFAPGRTAPEMRSAFNATAIENISANLPLPSFFYQNH 477
QY 261 -----EERVRPMPFPPTFLYTSQWEDPEPDMVEINPKDVTLTLSGGCNALNLVQ 314

Db 478 HWRIYYDDOLPKHTQFNDEYIYAFTHWDSRVDRBELNLGPDVVLTAITSAGDNILSYLMQ 537
Qy 315 GAGQVSVDCNPAQALLKKVAIQOLEFEDVWOLFGEVHPRIEELYEKLAFLPLFSQT 374
Db 538 SPARVHAILDNLPAQNHLLEKLVASFTTLDYPDVWKIFGEGKHPDFRSLLSKLSPHLSGR 597
Qy 375 SHNFSKRLWFO---HGLYYQGMKLCWLQCLAVVLGLGKTVKRLANAPTMEBQR 430
Db 598 AFQYWLNAHIFTDPAGRLGTYDTSGRVAIRFRWISTLFFCRSARVRLSLSTFTLEGORS 657
Qy 431 LWDNMLHFVKNQPKPLVWLVKVS-LVLPNKAVLWFGGVPKQVVALIKAD-----483
Db 658 IYHTKI-----RPC---LLNRFVNGVLSSDAFLMSALGVKNQVAMHEADYHRSI 706
Qy 484 -----GPIENYIARTMDGVAENSHVRKQNYFYNYCLTGKFLRDNCPITYLR 529
Db 707 SSTTSPSSKEKPSRAEAILHYTTSLDPLVSTSHLASDNPYLVGVLGQYTRQCHPDYLS 766
Qy 530 EAAFAATLKS-GVVDNLTVSTNFFMEEL---KARTYTKVILMDHVDWLDMP-----575
Db 767 PAHSILSAGPAGDGLRIHTDSIQEVLARFQPGTLTVAVWVDSMDWFDPPSPSEESKEGRG 826
Qy 576 VANELAECLAKQVAPGGIVWRSASISPPYAEILQKAGFDVRCI-----RRATQGYMDRV 630
Db 827 KAREQVRLNRLALKVGGKVLRSAGVEPWYVRFVVEGFGARRVCGRESGRGDQECIDRV 886
Qy 631 NMYSSFYMAR 641
Db 887 NMYASCWILEK 897

RESULT 4

US-10-118-495-3

; Sequence 3, Application US/10118495

; Publication No. US20030074688A1

; GENERAL INFORMATION:

; APPLICANT: Benning, Christoph

; APPLICANT: Riekhof, Wayne

; APPLICANT: Klug, Rouven

; TITLE OF INVENTION: Compositions and Methods for the Production of Betaine Lipids

; CURRENT APPLICATION NUMBER: US/10/118,495

; CURRENT FILING DATE: 2002-04-08

; PRIOR APPLICATION NUMBER: 60/283,812

; PRIOR FILING DATE: 2001-04-13

; NUMBER OF SEQ ID NOS: 42

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 3

; LENGTH: 416

; TYPE: PRT

; ORGANISM: Rhodobacter sphaeroides

US-10-118-495-3

Query Match 11.0%; Score 379.5; DB 4; Length 416;
Best Local Similarity 28.1%; Pred. No. 8.3e-29;
Matches 127; Conservative 68; Mismatches 182; Indels 75; Gaps 20;
Qy 231 TQGSIPYVWLRAPYVWIGRLPSVGHALH-----EERVERPPMPPTF---LYTQSW 280
Db 2 TQFALTHLP---APP---VAR---QIGAAVHRTSLLSASGLMER--MFSRLFHGLVYPOIW 51
Qy 281 EDPEPDMVEINPKDVTTLTSGGCNALNLVQAGQVSVDCNPAQSALLELKKVAIQ 340
Db 52 EDPVDMAAALAIRPGDRLVAIASGCGNVLSYLTQPGSILAVDLSPAVALGRKLAAAR 111
Qy 341 QL-BFEDVWOLFGEVHPRIEELYEKLAFLPLFSQTSNFW-----SKRLWYFQHGLYYQ 393
Db 112 TLPDHAAPFDLFGRADLPGNAALYDRHTAPALDGRSRYWEARSFPFGRRIQLFERGFYRH 171
Qy 394 GGMKLCWLQCLAVVLGLGKTVKRLANAPTMEBQRRLWDSNMLHFVKNQPKPLVWLVF 453
Db 172 GALGRFIGAANTLA---RAAGTDLRGFLDCPDIEAQRSPFYAHI-----GP-----LFE 217
Qy 454 KFSVLVFNKAVLWFGGVPKQVVALIKADG---IPIENYIARTMDGVAENSH-----503
Db 218 APVVOALARRPAALFGLGIPPAQYALLAGDGDGDLVPV-----LRORLHRLLCDF 267
Qy 504 VRKQNYFYNYCLTGKFLRDN---CPTYLREAAFAATLKSQVVDNLTVSTNFFMEELKARTY 560
Db 268 PLRENYFAFOAIARYPFPGEGALPPYLEPTAFETLREN-AGRVOIENRSLTEALAAEPE 326
Qy 561 TKV---ILMDHVDWLDMPVANELAECLAKQVAPGGIVWIR---SASLSPPYAEILQKAGF 614
Db 112 TLPDHAAPFDLFGRADLPGNAALYDRHTAPALDGRSRYWEARSFPFGRRIQLFERGFYRH 171
Qy 394 GGMKLCWLQCLAVVLGLGKTVKRLANAPTMEBQRRLWDSNMLHFVKNQPKPLVWLVF 453
Db 172 GALGRFIGAANTLA---RAAGTDLRGFLDCPDIEAQRSPFYAHI-----GP-----LFE 217

Qy 454 KFSVLVFNKAVLWFGGVPKQVVALIKADG---IPIENYIARTMDGVAENSH-----503
Db 218 APVVOALARRPAALFGLGIPPAQYALLAGDGDGDLVPV-----LRORLHRLLCDF 267
Qy 504 VRKQNYFYNYCLTGKFLRDN---CPTYLREAAFAATLKSQVVDNLTVSTNFFMEELKARTY 560
Db 268 PLRENYFAFOAIARYPFPGEGALPPYLEPTAFETLREN-AGRVOIENRSLTEALAAEPE 326
Qy 561 TKV---ILMDHVDWLDMPVANELAECLAKQVAPGGIVWIR---SASLSPPYAEILQKAGF 614
Db 327 ESIHGFTLLDAQDWMWTDALTLNRQVTRTAAPGARVIFRTGGAADLLP--GRVPEEILG 384
Qy 615 DVCIRRTAQG--YMDRVNMYSSFYMAR 644
Db 385 HWRADRAAQAGHAADRSIYGGFHLRYRRDA 416

RESULT 5

US-10-620-914-3

; Sequence 3, Application US/10620914

; Publication No. US20040093639A1

; GENERAL INFORMATION:

; APPLICANT: Benning, Christoph

; APPLICANT: Riekhof, Wayne

; APPLICANT: Klug, Rouven

; TITLE OF INVENTION: Compositions and Methods for the Production of Betaine Lipids

; FILE REFERENCE: MSU-07769

; CURRENT APPLICATION NUMBER: US/10/620,914

; CURRENT FILING DATE: 2003-07-16

; PRIOR APPLICATION NUMBER: 10/118,495

; PRIOR FILING DATE: 2002-04-08

; NUMBER OF SEQ ID NOS: 52

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 3

; LENGTH: 416

; TYPE: PRT

; ORGANISM: Rhodobacter sphaeroides

US-10-620-914-3

Query Match 11.0%; Score 379.5; DB 4; Length 416;
Best Local Similarity 28.1%; Pred. No. 8.3e-29;
Matches 127; Conservative 68; Mismatches 182; Indels 75; Gaps 20;
Qy 231 TQGSIPYVWLRAPYVWIGRLPSVGHALH-----EERVERPPMPPTF---LYTQSW 280
Db 2 TQFALTHLP---APP---VAR---QIGAAVHRTSLLSASGLMER--MFSRLFHGLVYPOIW 51
Qy 281 EDPEPDMVEINPKDVTTLTSGGCNALNLVQAGQVSVDCNPAQSALLELKKVAIQ 340
Db 52 EDPVDMAAALAIRPGDRLVAIASGCGNVLSYLTQPGSILAVDLSPAVALGRKLAAAR 111
Qy 341 QL-BFEDVWOLFGEVHPRIEELYEKLAFLPLFSQTSNFW-----SKRLWYFQHGLYYQ 393
Db 112 TLPDHAAPFDLFGRADLPGNAALYDRHTAPALDGRSRYWEARSFPFGRRIQLFERGFYRH 171
Qy 394 GGMKLCWLQCLAVVLGLGKTVKRLANAPTMEBQRRLWDSNMLHFVKNQPKPLVWLVF 453
Db 172 GALGRFIGAANTLA---RAAGTDLRGFLDCPDIEAQRSPFYAHI-----GP-----LFE 217
Qy 454 KFSVLVFNKAVLWFGGVPKQVVALIKADG---IPIENYIARTMDGVAENSH-----503
Db 218 APVVOALARRPAALFGLGIPPAQYALLAGDGDGDLVPV-----LRORLHRLLCDF 267
Qy 504 VRKQNYFYNYCLTGKFLRDN---CPTYLREAAFAATLKSQVVDNLTVSTNFFMEELKARTY 560
Db 268 PLRENYFAFOAIARYPFPGEGALPPYLEPTAFETLREN-AGRVOIENRSLTEALAAEPE 326
Qy 561 TKV---ILMDHVDWLDMPVANELAECLAKQVAPGGIVWIR---SASLSPPYAEILQKAGF 614
Db 327 ESIHGFTLLDAQDWMWTDALTLNRQVTRTAAPGARVIFRTGGAADLLP--GRVPEEILG 384
Qy 615 DVCIRRTAQG--YMDRVNMYSSFYMAR 644


```
Db 385 HWRADRAAGAGHAADRSAYGGFHLRYRRDA 416

RESULT 6
US-10-118-495-29
; Sequence 29, Application US/10118495
; Publication No. US20030074688A1
; GENERAL INFORMATION:
; APPLICANT: Benning, Christoph
; APPLICANT: Riekhof, Wayne
; APPLICANT: Klug, Rouven
; TITLE OF INVENTION: Compositions and Methods for the Production of Betaine Lipids
; FILE REFERENCE: MSU-06897
; CURRENT APPLICATION NUMBER: US/10/118,495
; CURRENT FILING DATE: 2002-04-08
; PRIOR APPLICATION NUMBER: 60/283,812
; PRIOR FILING DATE: 2001-04-13
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 29
; LENGTH: 416
; TYPE: PRT
; ORGANISM: Agrobacterium tumefaciens
US-10-118-495-29

Query Match 9.4%; Score 326.5; DB 4; Length 416;
Best Local Similarity 27.8%; Pred. No. 1.9e-23;
Matches 111; Conservative 69; Mismatches 158; Indels 61; Gaps 16;

Qy 275 LYTSWEDPEPDMEVMEINPKDVTLTSGGCNALLVQAGQVSVDCNPAQSALLEL 334
Db 44 VYQIWEDEPDMEAMELGEGHRIVTIGSGGCNMLAYLSRNPASIDVVDLNPHHIALNKL 103
Qy 335 KKVAIQQL-EPEDVQVLFGEVHPRIEELYEKKLAPFLSQTSHNFWSK-----RLWYF 386
Db 104 KLAAPRHLPAHQDVVRHFGRAGRTRSNVGYDFIAEHLDAITTKAYWSKRTLSGRRRISVF 163
Qy 387 QHGLYYQGGMGKLCWVLOCLAVLGLKTVKRLANAPTEBQRRLWDSNMLIHVFVKNPK 446
Db 164 DRNIYRTGLGRFGTGAHIMARLHGVLKLT--EMAKTRTLDEQRFDSKVAPLF----DK 217
Qy 447 PLV-WLFVKFVSLVLFNKAVLWFGGVPKGQY---ALIKADGIPYENIARTMDGVAENS 502
Db 218 PVVRWLTWRKSSSL-----FGLGIPPRQYDELASLSSDG-TVASVLKERLEKLCACNF 267
Qy 503 HVRKQNYFYNNCLTGKFLRDN---CPTYLRBAAPATLKSQVVDNLTVTSTNFFMEELK--- 556
Db 268 PL-SDNYFAWQAFARRYPEPEHGAIPAYLKPEYKEKIRNNTA-RVAVHHATYTELLSRKP 325
Qy 557 ARTYTKVILMDHVDWLDMPVANELAECLAKQVAPGGIVWRSAS-----LSPPYAEL 608
Db 326 ANGVDRIYLLDAQDMWTDVQLNELWSQISRTAASGARVIFRTAAEKSVIEGRLSP----- 380
Qy 609 IQKAGFDVR-----CIRRATO-GYMDRVNMYSSFYMAR 641
Db 381 -----DIRNQWVYLEERSNELNAMDRSAYGGFHIYOR 413

RESULT 7
US-10-620-914-29
; Sequence 29, Application US/10620914
; Publication No. US20040093639A1
; GENERAL INFORMATION:
; APPLICANT: Benning, Christoph
; APPLICANT: Riekhof, Wayne
; APPLICANT: Klug, Rouven
; TITLE OF INVENTION: Compositions and Methods for the Production of Betaine Lipids
; FILE REFERENCE: MSU-07769
; CURRENT APPLICATION NUMBER: US/10/620,914
; CURRENT FILING DATE: 2003-07-16
; PRIOR APPLICATION NUMBER: 10/118,495
; PRIOR FILING DATE: 2002-04-08
; NUMBER OF SEQ ID NOS: 52
```

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; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 29
; LENGTH: 416
; TYPE: PRT
; ORGANISM: Agrobacterium tumefaciens
US-10-620-914-29

Query Match 9.4%; Score 326.5; DB 4; Length 416;
Best Local Similarity 27.8%; Pred. No. 1.9e-23;
Matches 111; Conservative 69; Mismatches 158; Indels 61; Gaps 16;

Qy 275 LYTSWEDPEPDMEVMEINPKDVTLTSGGCNALLVQAGQVSVDCNPAQSALLEL 334
Db 44 VYQIWEDEPDMEAMELGEGHRIVTIGSGGCNMLAYLSRNPASIDVVDLNPHHIALNKL 103
Qy 335 KKVAIQQL-EPEDVQVLFGEVHPRIEELYEKKLAPFLSQTSHNFWSK-----RLWYF 386
Db 104 KLAAPRHLPAHQDVVRHFGRAGRTRSNVGYDFIAEHLDAITTKAYWSKRTLSGRRRISVF 163
Qy 387 QHGLYYQGGMGKLCWVLOCLAVLGLKTVKRLANAPTEBQRRLWDSNMLIHVFVKNPK 446
Db 164 DRNIYRTGLGRFGTGAHIMARLHGVLKLT--EMAKTRTLDEQRFDSKVAPLF----DK 217
Qy 447 PLV-WLFVKFVSLVLFNKAVLWFGGVPKGQY---ALIKADGIPYENIARTMDGVAENS 502
Db 218 PVVRWLTWRKSSSL-----FGLGIPPRQYDELASLSSDG-TVASVLKERLEKLCACNF 267
Qy 503 HVRKQNYFYNNCLTGKFLRDN---CPTYLRBAAPATLKSQVVDNLTVTSTNFFMEELK--- 556
Db 268 PL-SDNYFAWQAFARRYPEPEHGAIPAYLKPEYKEKIRNNTA-RVAVHHATYTELLSRKP 325
Qy 557 ARTYTKVILMDHVDWLDMPVANELAECLAKQVAPGGIVWRSAS-----LSPPYAEL 608
Db 326 ANGVDRIYLLDAQDMWTDVQLNELWSQISRTAASGARVIFRTAAEKSVIEGRLSP----- 380
Qy 609 IQKAGFDVR-----CIRRATO-GYMDRVNMYSSFYMAR 641
Db 381 -----DIRNQWVYLEERSNELNAMDRSAYGGFHIYOR 413

RESULT 8
US-10-118-495-41
; Sequence 41, Application US/10118495
; Publication No. US20030074688A1
; GENERAL INFORMATION:
; APPLICANT: Benning, Christoph
; APPLICANT: Riekhof, Wayne
; APPLICANT: Klug, Rouven
; TITLE OF INVENTION: Compositions and Methods for the Production of Betaine Lipids
; FILE REFERENCE: MSU-06897
; CURRENT APPLICATION NUMBER: US/10/118,495
; CURRENT FILING DATE: 2002-04-08
; PRIOR APPLICATION NUMBER: 60/283,812
; PRIOR FILING DATE: 2001-04-13
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 41
; LENGTH: 415
; TYPE: PRT
; ORGANISM: Mesorhizobium loti
US-10-118-495-41

Query Match 9.3%; Score 321; DB 4; Length 415;
Best Local Similarity 26.2%; Pred. No. 6.7e-23;
Matches 113; Conservative 70; Mismatches 178; Indels 72; Gaps 18;

Qy 255 VGHALHEERV-----ERPPMFPPTF---LYTSWEDPEPDMEVMEINPKDVTLTSG 304
Db 16 VGVAYQNRALS KAGISER--LFAFLFSLVYPIQWEDPDVDMQWQGLQGHRIVTIASG 73
Qy 305 GCNALLVQAGQVSVDCNPAQSALLEKVAIQQLFEF-DVMQVLFGEVHPRIEELY 363
Db 74 GCNIIAYLTRSPARIDAVDLNNAHIALNRMLKLEAVRRLPSQGDLPFRFFGAADTSHNSQAY 133
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Qy 364 EKXAPFISQTSNFWSKRLM-----YFOHGLYYQGMGKLCWVLOCLAVVLG----- 411
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 134 DRFTAPHLDPVSRHYWERNRGRRIIAVFORNFYQTGLLG-----LFIAMGHRTAK 185
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 412 -LGKTVKRLANAPTMEEORRLWDSNMLIHFVKNGKPLVLFVKSIVLNFKNKAVLWFGG 470
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 186 FFGVNPAMHMEARNIGEORRFNEELAPVFDK---KLLKWATSRKASL-----FGL 233
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 471 GVPKQY--ALIKADGPIENYIAR---TMDGVAENSHVRKQNYFYNYNCLTGKFLRDN- 523
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 234 GIPPAQYDSLITSGDGTWASVLKARLEKACDPFLEN-----NYFAWQAFARVPNPEGE 287
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 524 --CPTYLREAAFATLKSGVDNLTVSTNFFMEEL---KARTYTKVILMDHVDWLDMPVAN 578
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 288 AALPAYLEKQNYETIR-GNIDRVAIHHLNLIIEFLAGKDGAGTVDRFILLDAQDMMTDDQLN 346
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 579 ELAECLAQKQVAPGGIVWRS---SLSP--PYAEIIOKAGFVRCIRATQGYMDRVNMY 633
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 347 ALMSEISRTASAGARVIFRTAAEPSLLPGRVSTSLDDQMDYQDEASREFSA--RDRSAIY 404
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 634 SSFYMARCKGA 644
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 405 GGFHLYVKRTA 415
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 9
US-10-620-914-41
; Sequence 41, Application US/10620914
; Publication No. US20040093639A1
; GENERAL INFORMATION:
; APPLICANT: Benning, Christoph
; APPLICANT: Riekhof, Wayne
; APPLICANT: Klug, Rouven
; TITLE OF INVENTION: Compositions and Methods for the Production of Betaine Lipids
; FILE REFERENCE: MSU-07769
; CURRENT APPLICATION NUMBER: US/10/620,914
; CURRENT FILING DATE: 2003-07-16
; PRIOR APPLICATION NUMBER: 10/118,495
; PRIOR FILING DATE: 2002-04-08
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 41
; LENGTH: 415
; TYPE: PRT
; ORGANISM: Mesorhizobium loti
US-10-620-914-41

Query Match 9.3%; Score 321; DB 4; Length 415;
Best Local Similarity 26.2%; Pred. No. 6.7e-23;
Matches 113; Conservative 70; Mismatches 176; Indels 72; Gaps 16;

Qy 255 VGHALHEERV-----ERPMPFPTF---LYTOSWEDPEPDMVMEINPKDVTLTLSG 304
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 16 VGKAVYQNRALSAGISER--LFAFLFGLYPIQWEDPDVDMQAMQGGHRIIVTASG 73
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 305 GCNALNLLVQAGQVSDNCNPAQSALLEKKAIVQIQLEFE-DVMQFLGEGVHPRIEBELY 363
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 74 GCNLAIVLTRSPARIDAVDNAIALNRMKLEAVRPLPSQGLDFRFPFGAADTSHNSQAY 133
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 364 EKXAPFISQTSNFWSKRLM-----YFOHGLYYQGMGKLCWVLOCLAVVLG----- 411
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 134 DRFTAPHLDPVSRHYWERNRGRRIIAVFORNFYQTGLLG-----LFIAMGHRTAK 185
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 412 -LGKTVKRLANAPTMEEORRLWDSNMLIHFVKNGKPLVLFVKSIVLNFKNKAVLWFGG 470
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 186 FFGVNPAMHMEARNIGEORRFNEELAPVFDK---KLLKWATSRKASL-----FGL 233
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 471 GVPKQY--ALIKADGPIENYIAR---TMDGVAENSHVRKQNYFYNYNCLTGKFLRDN- 523
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 234 GIPPAQYDSLITSGDGTWASVLKARLEKACDPFLEN-----NYFAWQAFARVPNPEGE 287
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 524 --CPTYLREAAFATLKSGVDNLTVSTNFFMEEL---KARTYTKVILMDHVDWLDMPVAN 578
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

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Db 288 AALPAYLEKQNYETIR-GNIDRVAIHHLNLIIEFLAGKDGAGTVDRFILLDAQDMMTDDQLN 346
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 579 ELAECLAQKQVAPGGIVWRS---SLSP--PYAEIIOKAGFVRCIRATQGYMDRVNMY 633
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 347 ALMSEISRTASAGARVIFRTAAEPSLLPGRVSTSLDDQMDYQDEASREFSA--RDRSAIY 404
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 634 SSFYMARCKGA 644
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 405 GGFHLYVKRTA 415
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 10
US-10-118-495-33
; Sequence 33, Application US/10118495
; Publication No. US20030074688A1
; GENERAL INFORMATION:
; APPLICANT: Benning, Christoph
; APPLICANT: Riekhof, Wayne
; APPLICANT: Klug, Rouven
; TITLE OF INVENTION: Compositions and Methods for the Production of Betaine Lipids
; FILE REFERENCE: MSU-06897
; CURRENT APPLICATION NUMBER: US/10/118,495
; CURRENT FILING DATE: 2002-04-08
; PRIOR APPLICATION NUMBER: 60/283,812
; PRIOR FILING DATE: 2001-04-13
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 33
; LENGTH: 416
; TYPE: PRT
; ORGANISM: Sinorhizobium meliloti
US-10-118-495-33

Query Match 8.4%; Score 292.5; DB 4; Length 416;
Best Local Similarity 26.0%; Pred. No. 5.1e-20;
Matches 102; Conservative 71; Mismatches 174; Indels 45; Gaps 16;

Qy 275 LYTOSWEDPEPDMVMEINPKDVTLTLSGDCNALNLLVQAGQVSDNCNPAQSALLEL 334
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 45 VYQIWEDPIVDMQAMQIRPGHRIIVTIGSGGCNMLTVLSAEPARIDVVDLNPHTALNRL 104
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 335 KKVAIQQL-EFEDVWQLFG-BGVHPRIEBELYEKKLAPLSQTSNFWSD-----KRLWY 385
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 105 KLSAFRHLPSHKDYVRELAIVEGTRTN-GQAYDVFLAPKLDPATRAYWNGRDLTGRRRIGV 163
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 386 FQHGLYYQGMGKLCWVLOCLAVVLGKTKVRLANAPTMEEORRLWDSNMLIHFVKNGP 445
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 164 FGRNVYTGTLGRFISASHALARLHGPN--EDFVKARSMREQQFFDDKLAFLP-----E 217
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 446 KPLV-WLFFVFSVLNFKNKAVLWFGGVGVPDKQYALIKADGPIENYIARTMDGVAENSHV 504
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 218 RPVIRWITSRSSL-----FGLGIPPOQFDELAS--LSREKSVAAVLNRLEKLTLC 266
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 505 R---KQNYFYNYNCLTGKFLRDN---CPTYLREAAFATLKSGVDNLTVSTNFFMEEL--- 555
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 267 HFPLRDNYFAWQAFARVPNPEGEGLPPYQLQASRYEARIDN-ABRVEVHHASFTELLAGK 325
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 556 KARTYTKVILMDHVDWLDMPVANLEAELAKQVAPGGIVWRS---ASLSP--YAEILIQ 610
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 326 PAASVDRYLLDAQDMMTDDQLNDLWTEITRTADAGAVVIFRTAAEASILPRLSTLLD 385
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 611 KAGFVRCIRATQGYMDRVNMYSSFYMARCK 642
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 386 QWYDAETSMEL--GAEDRSALYGGFHYRCK 415
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 11
US-10-620-914-33
; Sequence 33, Application US/10620914
; Publication No. US20040093639A1
; GENERAL INFORMATION:
; APPLICANT: Benning, Christoph

```



```

Matches 141; Conservative 79; Mismatches 217; Indels 240; Gaps 35;
QY 107 HSLCEVAKKAKAK-GWRNVQVVEADACOPAPPEGTATLITFSYSG----- 150
Db 422 HNL-----KAAKAKLGYDPVELDPEDMCRMA-TEQPQTATVSVSDAVATYLYKYYHP 476
QY 151 -----LTMPPFH-NVI-----DQACSYLSQDGLGVVA 177
Db 477 FIFALCTIIPMEPDEVLRKSGTLCALLMVOAFHANIIFPNKQOEFNKLTDDGHVLDNA 536
QY 178 DFYVSG-----KYDLP--LROMPWSRRFFWRSIFDIDNIDIGPERRAYLEO--KL 223
Db 537 ETVVGGHVEALESYGFRSDIPCRFRMNAAPDFLLORVEKTKWHAIEEEKVPVQATNF 596
QY 224 ERVWEQ--NTQGSIPYVWMLRAPYYVWIGRLPSVGHALHEERVERP-----PMFPPT 273
Db 597 QEVCEQIKTKLTSKQVP-----NRIECPLIYVHLDVGAMYENI 634
QY 274 FLYTQSWEDPEDMEVMEINPKDVTILTSGCCN-----ALNLLVQAGQVVSVDN 325
Db 635 ILTNR-----LQPSAIVDEATCAACDFNKFCASCQKQKQWQWRGEFM----- 676
QY 326 PAQSALLEKKVAIOQLFEDVWOLFGRGVHPRIEEL-----YEK-KLAPP----- 370
Db 677 PASRS--EYHRIO-HOLESEKFPPLFPEGAPAFHELSEBOAKYKRRRLADYCKYAKK 733
QY 371 -----LSQTSNFWKRLWYFQHGGLYQGGMGKLCWVLQCLAVVLGLGKTVKR 418
Db 734 IHVTKVEERLITICQRENSFYVDTVRAFDRDRYEFKGLHWKVKKLSAAVEGDASEVKR 793
QY 419 LANAPTMEEQRLWDSNMLIH-----FVKNQPKPLVWLFWKFSVLVLFNKAVLWF 468
Db 794 CKN-----MEILYDSLQLAHKCILNSFYGYMYRKGAR--WYSMEMAGIVCFT----- 838
QY 469 GGVPGKQYALIKADGIPI-----ENVIARTMDGVAENSHVRKNQYFY 512
Db 839 GANITQARELIEQIGRPLELTDGICWVLPNSFFENFVIKT-----TNKKPKLTISYP 893
QY 513 NCLTGKFLRDNCTY-----LREAAFATLKSGVVDNLTVSTNFFMBELKARTYTYKVLMDH 568
Db 894 GAMLNIMVKEGFTNHQYQELTEPSSLTY-----VTHSENSIPEVDG-PYLAMIL--- 942
QY 569 VDWLDMPVANLAECLAKQVAPGGIVWRSLSLSPYAEILQKAGFDVRCIRRTATQGYMD 628
Db 943 -----PASKEEGKKLKRYYA-----VFNEDGSL-----AEL---KGFEVK-----RRGELQ 980
QY 629 RVNMY-SSFYMWARRKGA 644
Db 981 LKIFQSSVFEAFUKGS 997

RESULT 14
; Sequence 35, Application US/10118495
; Publication No. US20030074688A1
; GENERAL INFORMATION:
; APPLICANT: Benning, Christoph
; APPLICANT: Riekhof, Wayne
; APPLICANT: Klug, Rouven
; TITLE OF INVENTION: Compositions and Methods for the Production of Betaine Lipids
; FILE REFERENCE: MSU-06897
; CURRENT APPLICATION NUMBER: US/10/118,495
; PRIOR FILING DATE: 2002-04-08
; PRIOR FILING DATE: 2001-04-13
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 35
; LENGTH: 221
; TYPE: PRT
; ORGANISM: Sinorhizobium meliloti
US-10-118-495-35

Matches 141; Conservative 79; Mismatches 217; Indels 240; Gaps 35;
QY 107 HSLCEVAKKAKAK-GWRNVQVVEADACOPAPPEGTATLITFSYSG----- 150
Db 422 HNL-----KAAKAKLGYDPVELDPEDMCRMA-TEQPQTATVSVSDAVATYLYKYYHP 476
QY 151 -----LTMPPFH-NVI-----DQACSYLSQDGLGVVA 177
Db 477 FIFALCTIIPMEPDEVLRKSGTLCALLMVOAFHANIIFPNKQOEFNKLTDDGHVLDNA 536
QY 178 DFYVSG-----KYDLP--LROMPWSRRFFWRSIFDIDNIDIGPERRAYLEO--KL 223
Db 537 ETVVGGHVEALESYGFRSDIPCRFRMNAAPDFLLORVEKTKWHAIEEEKVPVQATNF 596
QY 224 ERVWEQ--NTQGSIPYVWMLRAPYYVWIGRLPSVGHALHEERVERP-----PMFPPT 273
Db 597 QEVCEQIKTKLTSKQVP-----NRIECPLIYVHLDVGAMYENI 634
QY 274 FLYTQSWEDPEDMEVMEINPKDVTILTSGCCN-----ALNLLVQAGQVVSVDN 325
Db 635 ILTNR-----LQPSAIVDEATCAACDFNKFCASCQKQKQWQWRGEFM----- 676
QY 326 PAQSALLEKKVAIOQLFEDVWOLFGRGVHPRIEEL-----YEK-KLAPP----- 370
Db 677 PASRS--EYHRIO-HOLESEKFPPLFPEGAPAFHELSEBOAKYKRRRLADYCKYAKK 733
QY 371 -----LSQTSNFWKRLWYFQHGGLYQGGMGKLCWVLQCLAVVLGLGKTVKR 418
Db 734 IHVTKVEERLITICQRENSFYVDTVRAFDRDRYEFKGLHWKVKKLSAAVEGDASEVKR 793
QY 419 LANAPTMEEQRLWDSNMLIH-----FVKNQPKPLVWLFWKFSVLVLFNKAVLWF 468
Db 794 CKN-----MEILYDSLQLAHKCILNSFYGYMYRKGAR--WYSMEMAGIVCFT----- 838
QY 469 GGVPGKQYALIKADGIPI-----ENVIARTMDGVAENSHVRKNQYFY 512
Db 839 GANITQARELIEQIGRPLELTDGICWVLPNSFFENFVIKT-----TNKKPKLTISYP 893
QY 513 NCLTGKFLRDNCTY-----LREAAFATLKSGVVDNLTVSTNFFMBELKARTYTYKVLMDH 568
Db 894 GAMLNIMVKEGFTNHQYQELTEPSSLTY-----VTHSENSIPEVDG-PYLAMIL--- 942
QY 569 VDWLDMPVANLAECLAKQVAPGGIVWRSLSLSPYAEILQKAGFDVRCIRRTATQGYMD 628
Db 943 -----PASKEEGKKLKRYYA-----VFNEDGSL-----AEL---KGFEVK-----RRGELQ 980
QY 629 RVNMY-SSFYMWARRKGA 644
Db 981 LKIFQSSVFEAFUKGS 997

RESULT 14
; Sequence 35, Application US/10118495
; Publication No. US20030074688A1
; GENERAL INFORMATION:
; APPLICANT: Benning, Christoph
; APPLICANT: Riekhof, Wayne
; APPLICANT: Klug, Rouven
; TITLE OF INVENTION: Compositions and Methods for the Production of Betaine Lipids
; FILE REFERENCE: MSU-06897
; CURRENT APPLICATION NUMBER: US/10/118,495
; PRIOR FILING DATE: 2002-04-08
; PRIOR FILING DATE: 2001-04-13
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 35
; LENGTH: 221
; TYPE: PRT
; ORGANISM: Sinorhizobium meliloti
US-10-118-495-35

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Query Match 3.5%; Score 120; DB 4; Length 221;
Best Local Similarity 24.1%; Pred. No. 0.0051;
Matches 39; Conservative 34; Mismatches 67; Indels 22; Gaps 6;
QY 75 VDLGGGTGENVDMADYIDLAKFKSIYVVDLCHSLCEVAKKAKAKGWNQVQVVEADACQ 134
Db 53 LEVCGGTGRNLAVIGDLYPGAR---LFGLDISAEMLATAKAKLRRQNRPDVLRVADATN 109
QY 135 FA-----PPEGTATLITFSYSLTMIPTPHNVIDQACSYLSQDGLGVVADFYVSGKYDLP 190
Db 110 FTAASFQOEGFDRIV-ISYALSMVPEWEKAVDAATAALKPGGSLHIADFGQOEGWPAGFR 168
QY 191 Q--MPWSRRFF---WRSIFDIDN-----IDIGPERRAY 218
Db 169 RFLQAWLRFRFHTPRETLFDVWKRKAERNDAALVRSLSRGY 210

RESULT 15
US-10-620-914-35
; Sequence 35, Application US/10620914
; Publication No. US20040093639A1
; GENERAL INFORMATION:
; APPLICANT: Benning, Christoph
; APPLICANT: Riekhof, Wayne
; APPLICANT: Klug, Rouven
; TITLE OF INVENTION: Compositions and Methods for the Production of Betaine Lipids
; FILE REFERENCE: MSU-07769
; CURRENT APPLICATION NUMBER: US/10/620,914
; CURRENT FILING DATE: 2003-07-16
; PRIOR APPLICATION NUMBER: 10/118,495
; PRIOR FILING DATE: 2002-04-08
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 35
; LENGTH: 221
; TYPE: PRT
; ORGANISM: Sinorhizobium meliloti
US-10-620-914-35

Query Match 3.5%; Score 120; DB 4; Length 221;
Best Local Similarity 24.1%; Pred. No. 0.0051;
Matches 39; Conservative 34; Mismatches 67; Indels 22; Gaps 6;
QY 75 VDLGGGTGENVDMADYIDLAKFKSIYVVDLCHSLCEVAKKAKAKGWNQVQVVEADACQ 134
Db 53 LEVCGGTGRNLAVIGDLYPGAR---LFGLDISAEMLATAKAKLRRQNRPDVLRVADATN 109
QY 135 FA-----PPEGTATLITFSYSLTMIPTPHNVIDQACSYLSQDGLGVVADFYVSGKYDLP 190
Db 110 FTAASFQOEGFDRIV-ISYALSMVPEWEKAVDAATAALKPGGSLHIADFGQOEGWPAGFR 168
QY 191 Q--MPWSRRFF---WRSIFDIDN-----IDIGPERRAY 218
Db 169 RFLQAWLRFRFHTPRETLFDVWKRKAERNDAALVRSLSRGY 210

Search completed: May 5, 2006, 07:51:03
Job time : 89 secs

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: May 5, 2006, 07:48:33 ; Search time 46 Seconds
(without alignments)
652.011 Million cell updates/sec

Title: US-10-620-914-45

Perfect score: 3463

Sequence: 1 MGSRDGRPSYTKKNFSLE.....RVNMYSSFYMARRKGAKDN 648

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 235405 seqs, 46284737 residues

Total number of hits satisfying chosen parameters: 235405

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA_New:
1: /SIDSS/prodata/1/pubpaa/US08_NEW_PUB.pep1.*
2: /SIDSS/prodata/1/pubpaa/US06_NEW_PUB.pep.*
3: /SIDSS/prodata/1/pubpaa/US07_NEW_PUB.pep.*
4: /SIDSS/prodata/1/pubpaa/US08_NEW_PUB.pep.*
5: /SIDSS/prodata/1/pubpaa/PCT_NEW_PUB.pep.*
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11: /SIDSS/prodata/1/pubpaa/US11_NEW_PUB.pep1.*
12: /SIDSS/prodata/1/pubpaa/US60_NEW_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	106	3.1	472	11 US-11-169-041-156	Sequence 156, App
2	106	3.1	684	11 US-11-079-463-7496	Sequence 7496, App
3	102	2.9	448	11 US-11-124-367A-282	Sequence 282, App
4	101.5	2.9	865	11 US-11-079-463-9886	Sequence 9886, App
5	101	2.9	588	11 US-11-079-463-7941	Sequence 7941, App
6	99	2.9	549	11 US-11-188-298-13759	Sequence 13759, A
7	97	2.8	2209	10 US-11-301-554-1903	Sequence 1903, App
8	96	2.8	326	9 US-10-467-657-7224	Sequence 7224, App
9	95.5	2.8	2890	11 US-11-115-639-31	Sequence 31, Appl
10	95.5	2.8	2890	11 US-11-115-639-32	Sequence 32, Appl
11	95.5	2.8	2890	11 US-11-115-639-33	Sequence 33, Appl
12	94	2.7	658	11 US-11-096-568A-2582	Sequence 2582, App
13	94	2.7	660	11 US-11-096-568A-2581	Sequence 2581, App
14	94	2.7	680	11 US-11-096-568A-2580	Sequence 2580, App
15	93.5	2.7	344	11 US-11-153-185-7	Sequence 7, Appl1
16	93.5	2.7	1197	9 US-10-055-877-8	Sequence 8, Appl1
17	93.5	2.7	1247	9 US-10-055-877-10	Sequence 10, Appl
18	93	2.7	417	11 US-11-098-686-11330	Sequence 11330, A
19	92.5	2.7	358	11 US-11-045-004-2727	Sequence 2727, App
20	92.5	2.7	1590	9 US-10-055-877-146	Sequence 146, App
21	92	2.7	316	11 US-11-096-568A-1265	Sequence 1265, App

22	92	2.7	477	11 US-11-079-463-9020	Sequence 9020, Ap
23	91.5	2.6	241	11 US-11-098-686-10262	Sequence 10262, A
24	91.5	2.6	389	11 US-11-079-463-8258	Sequence 8258, Ap
25	91	2.6	749	11 US-11-072-512-2622	Sequence 2622, Ap
26	90.5	2.6	1249	9 US-10-506-454-486	Sequence 486, App
27	89	2.6	537	11 US-11-109-156-28	Sequence 28, Appl
28	89	2.6	577	9 US-10-718-264-3	Sequence 3, Appl1
29	89	2.6	577	9 US-10-718-264-3	Sequence 3, Appl1
30	89	2.6	577	11 US-11-176-667-3	Sequence 376, App
31	88.5	2.6	329	11 US-11-234-786-376	Sequence 299, App
32	88.5	2.6	329	11 US-11-139-041-299	Sequence 299, App
33	88	2.5	217	11 US-11-188-298-9904	Sequence 1923, Ap
34	87.5	2.5	237	11 US-11-045-004-1923	Sequence 10005, A
35	87.5	2.5	834	11 US-11-087-099-10005	Sequence 14739, A
36	87.5	2.5	852	11 US-11-188-298-14739	Sequence 4, Appl1
37	87	2.5	243	11 US-11-153-185-4	Sequence 6590, Ap
38	87	2.5	265	9 US-10-467-657-6590	Sequence 7654, Ap
39	87	2.5	265	9 US-10-467-657-7654	Sequence 3, Appl1
40	87	2.5	335	11 US-11-153-185-3	Sequence 5, Appl1
41	87	2.5	338	11 US-11-153-185-5	Sequence 2, Appl1
42	87	2.5	339	11 US-11-153-185-2	Sequence 2180, Ap
43	87	2.5	565	11 US-11-072-512-2180	Sequence 664, App
44	86.5	2.5	395	9 US-10-793-626-664	Sequence 1573, Ap
45	86.5	2.5	431	9 US-10-506-454-1573	

ALIGNMENTS

RESULT 1
US-11-169-041-156
; Sequence 156, Application US/11169041
; Publication No. US20060019284A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: IDENTIFICATION OF POLYNUCLEOTIDES FOR PREDICTING ACTIVITY OF
; TITLE OF INVENTION: COMPOUNDS THAT INTERACT WITH AND/OR MODULATE PROTEIN TYROSINE
; TITLE OF INVENTION: KINASES AND/OR PROTEIN TYROSINE KINASE PATHWAYS IN LUNG CANCER
; TITLE OF INVENTION: CELLS
; FILE REFERENCE: 10001 NP
; CURRENT APPLICATION NUMBER: US/11/169,041
; CURRENT FILING DATE: 2005-06-28
; PRIOR APPLICATION NUMBER: 60/584,405
; PRIOR FILING DATE: 2004-06-30
; NUMBER OF SEQ ID NOS: 527
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 156
; LENGTH: 472
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-169-041-156

Query Match 3.1%; Score 106; DB 11; Length 472;
Best Local Similarity 20.4%; Pred. No. 0.22;
Matches 90; Conservative 54; Mismatches 155; Indels 142; Gaps 19;

QY	12	YTKNFSLEKILKLSMKDDLTVLRLHMFSGSKGGDHAA-----RLESFYGPOAA--AFAA 64
DB	39	PYRTEFQNRFEK-ATMNCNLAYLXHL-----KQNEALECLRKAELIQQEHADQAEIR 92
QY	65	RLAERSNLIWDLGGGTGENVDMADYID--LAKPKSIYVVDLCHSLCEVAKKKAKAGW 122
DB	93	SLVTWGNVAYYYHMGRLSDVQIYVDKVKHVCESFSPYRIESPELDCBEGWTRLCGGN 152
QY	123	KN--VQVVEADACQFAP---PEGTATLITFSYSLTWIPPHNVIDQACSVLSQDGLGVAD 178
DB	153	QNERAKVCFEALREKKPKNPEFTSGLATASRLONWPPSQNAID----- 196
QY	179	FVSGKYDLPLRQMPWSRRFFRSIFDIDNDIGDPER---RAYLEQKLERVWEQNTQGS1 235
DB	197	-----PLRQA-----IRLNPDNQYLKVLALKLHKHREE----- 225
QY	236	PYPWMLRAPYYVWIGRLPFSVGHALHEERVRPP-----MPPPTFLYTQSWEDPEPDMEV-- 289

Db 226 -----GEEGEGEKLVEALEKAPGVTVDVLSAAKPYRRKDEPDKAIELLK 271
Qy 290 --MEINPKDVTLTTSGCCNALNLVOGAGQVVSVDNCP--AQSALELKKVAIOQL--- 342
Db 272 KALEYIPNNAYLHCQIGCCYRAKVF-----QVMNLRENGMYGKRKLELIGHAVALKKA 326
Qy 343 -----EPEDWQLGEGVHPRIELEYEKKLAPFLSQTSH----- 376
Db 327 DEANDNLFRVCSILASLHALADQVEDABYF-----QKEFSKELTPVAKQLHLHRYG 378
Qy 377 NFW-----SKRLWYFOHGL 390
Db 379 NFQLYQMKCEDKAHHFIEGV 399
RESULT 2
US-11-079-463-7496
; Sequence 7496, Application US/11079463
; Publication No. US20060073161A1
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO BACTEROIDES FR
; FILE REFERENCE: PATH00-03DIV2
; CURRENT APPLICATION NUMBER: US/11/079,463
; CURRENT FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/128,705
; PRIOR FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: US 09/540,209
; PRIOR FILING DATE: 2000-04-04
; NUMBER OF SEQ ID NOS: 10444
; SEQ ID NO 7496
; LENGTH: 684
; TYPE: PRT
; ORGANISM: B. fragilis
US-11-079-463-7496
Query Match 3.1%; Score 106; DB 11; Length 684;
Best Local Similarity 20.1%; Pred. No. 0.38;
Matches 120; Conservative 70; Mismatches 218; Indels 188; Gaps 30;
Qy 127 VVEADACQAPPEGATLITFSYSLTM-----IppPHNVI---DOACSYSLSODGL 173
Db 13 VILLTACGAKKNTAEADNFYIVQFADQILRYRVPGENLTLOKELVYLTQAL 72
Qy 174 VGVAD--FYVSGKYDPLRQMPWSRRFFWRSIFDIDNIDIGERRAYLEQKLEWQON- 230
Db 73 EG-RDILFDQNGKYNLTIRM-----LETIYDTYDGRNSPDPVNLTTYLKRVWFSNG 124
Qy 231 ---TQGSIPYVWL-----RAPYVYWGRLPSVGHALHEERVR--PPMPPTFL----- 275
Db 125 IHHYGESEKFPVGFTEFLKQALLSVDASKPLAQOQTVEQLFEELSVPVFDPKVMPKRV 184
Qy 276 -----VTQSWDEPDPMEVMEI-----NPKDVTLTTSGCCNALNLVOGAGQV 319
Db 185 NOAGEDLVLTSASNYDGVTOQEEAEAFYNALKNPKDE--TPVSYGLN--SRLVKEDGKI 240
Qy 320 VSDCNPAQSALLELKKVAIOQLEFEDVWQLFGEVHPRIELEYEKKLAPFLSQTSHFW 379
Db 241 I-----EKWKVGG-----LYTQAEKIV-----YW 261
Qy 380 SKRLWYFOHGLYQGGMGKLCWVLOCLAVVLGLKTVK--RLANAPTMBEORRLW--DSN 435
Db 262 LKKA-----EG-----VAEDDAQKAIGKLIBEYETGDLKTFDEVAILMVKDLN 305
Qy 436 MLIHFVKN-----GPKPLVWLVFVSL-----VLFNKAVLWFGGVP--GKQVAL 479
Db 306 SRVDTNGFTSYGDPGLMKASWESIVNFKDLEARTRELITSSNAQWFDHSDSPVDKQFKK 365
Qy 480 IKADGIPIENYIARTMDGVAENSHVRKQNYFYNNCLTKGFLRDNCPYTLREAAFATLSG 539
Db 366 EKVKGVTAKVITAAITLG-----DLYPSTAIGINLPNSNWIRSHGS-----KSV 410

Qy 540 VVDNLT-----VSTNPFMEELKARTYTKVILMDHVDMLDMPVANELAECL---AKOVAP 590
Db 411 TIGNITDAYNKAAHNGFNEEFVYSDTEKQIDIKYAD--LTGELHTDHLHECLGHGSGKLLP 469
Qy 591 GGIWIRSASLSP-----PYABELIQAGFDPVRCIRRATQGYMDRVNMYSSFYMARRK 642
Db 470 G-----VDPDALKAYGSTIEEA-----RADLFLGLYYVADPK 500
RESULT 3
US-11-124-367A-282
; Sequence 282, Application US/11124367A
; Publication No. US20060024700A1
; GENERAL INFORMATION:
; APPLICANT: Michele Cargill
; APPLICANT: Hongjin Huang
; TITLE OF INVENTION: Genetic Polymorphisms Associated with
; FILE REFERENCE: CL001519.ORD
; CURRENT APPLICATION NUMBER: US/11/124,367A
; CURRENT FILING DATE: 2005-05-09
; PRIOR APPLICATION NUMBER: US 60/568,846
; PRIOR FILING DATE: 2004-05-07
; PRIOR APPLICATION NUMBER: US 60/582,609
; PRIOR FILING DATE: 2004-06-25
; PRIOR APPLICATION NUMBER: US 60/599,554
; PRIOR FILING DATE: 2004-08-09
; NUMBER OF SEQ ID NOS: 34460
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 282
; LENGTH: 448
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-124-367A-282

Query Match 2.9%; Score 102; DB 11; Length 448;
Best Local Similarity 20.8%; Pred. No. 0.47;
Matches 90; Conservative 54; Mismatches 163; Indels 126; Gaps 19;
Qy 12 YTKNFSLEKULKLSMKDDLTVLRLHMFWSKGGDHAA-----RLESFYGPOAA--AFAA 64
Db 15 FYRTEFQNRPEK-ATMNCNLLAYLAKHL-----KGQNEAALECLRKAEELIQEHADQAEIR 68
Qy 65 PLAERSNLIWDLGGGTGCVNMDMADYID--LAKFKSYVVDLCHSLCEVAKKAKAGW 122
Db 69 SLVTWGNVAYVYHNGRLSDQIYVDKVKHCEKFSPTRIESPELDCBEGWTRUKCGN 128
Qy 123 KN--VQVVEADACOFAP--PEGTATLITFSYSLTMIPPHNVIDQACSYSLSODGLGVAD 178
Db 129 QNERAKVCFEKALEKKPKNPEFTSGLAISYRLDNWPPSQNAID----- 172
Qy 179 FYVSGKYDPLRQMPWSRRFFWRSIFDIDNIDIGPER--RAYLEQKLEWQONQTSI 235
Db 173 -----PLROA-----IRLNPNOYLKVLALKLHOMREE----- 201
Qy 236 PYVPLRPYVYVWIGRLPSVGHALHEERVRPP-----MFPPTFLTQSWEDPEPMEV-- 289
Db 202 -----GEEGEGEKLVEALEKAPGVTVDVLSAAKPYRRKDEPDKAIELLK 247
Qy 290 --MEINPKDVTLTTSGCCNALNLVOGAGQVVSVDNCP--AQSALELKKVAIOQLEFE 345
Db 248 KALEYIPNNAYLHCQIGCCYRAKVF-----QVMNLRENGMYGKRKLELIGHAVALKKA 302
Qy 346 D-----VMQLFG-----EGVHPRIELEYEKKLAPFLSQTSH-----NFW----- 379
Db 303 DEANDNLFRVCSILASLHALADQVEAEYFYQKEFSKELTPVAKQLHLHRYGNYOMK 362
Qy 380 --SKELWYFOHGL 390
Db 363 CEDKAHHFIEGV 375

RESULT 4
US-11-079-463-9886
; Sequence 9886, Application US/11079463
; Publication No. US20060073161A1
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO BACTEROIDES FR
; FILE REFERENCE: PATH00-03DIV2
; CURRENT APPLICATION NUMBER: US/11/079,463
; CURRENT FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/128,705
; PRIOR FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: US 09/540,209
; PRIOR FILING DATE: 2000-04-04
; NUMBER OF SEQ ID NOS: 10444
; SEQ ID NO 9886
; LENGTH: 865
; TYPE: PRT
; ORGANISM: B.fragilis
US-11-079-463-9886

Query Match 2.9%; Score 101.5; DB 11; Length 865;
Best Local Similarity 19.0%; Pred. No. 1.4;
Matches 113; Conservative 68; Mismatches 181; Indels 233; Gaps 31;

Qy 124 NVQVEADACQAPPEGATLITFSYL-----TMIPPHNVIDQACSYLSQD 171
||| : : : : :
Db 296 NVQRI-----VATGLTFNQAIELVRASSLYTVHTVPVAGHDYD-----E 338
||| : : : : :
Qy 172 GLVGADFYVSGKYDLPURQWPWRRFFWRISFIDNIDIGPERRAYLEQKLERWEONT 231
||| : : : : :
Db 339 GLFGK-----YFVXMGISWDDLDLGRNPGDKG-----ERFCMSVFACNT 383
||| : : : : :
Qy 232 QGSIYPVPLRAPY-----YVWIGRLPSVGH-----ALH-----EERVERPPMPP 272
||| : : : : :
Db 384 SOEVNGSVLHGKVSQEMFSSIWKGYPPEESHVGVTVNGVHPPTWSATEWQOLYAKFNE 443
||| : : : : :
Qy 273 TFLYTQSWEDPEPDMVEINPKDVTLTSTGGCNALNLLVQGAGQVVSVDNCPAQSA 332
||| : : : : :
Db 444 NFLYDQS-----NPK-----IW 455
||| : : : : :
Qy 333 ELKKVAIQOLEFEDVWQLFGEVHPRIEELYEKKLAPFLSOTSNFWSKRLWYFQHGLY 392
||| : : : : :
Db 456 E-----AIYNVDEEIW-----KTRVTMKNKLVDYIRKQFRETWLN----- 492
||| : : : : :
Qy 393 QGGMGKLCWLQCL-----AVVLGLGKTVKRLANAPTMEEQRRLWDSNMLIHPVKNGPKPLV 449
||| : : : : :
Db 493 QGDSRIVSLDKINPNALLIGFRRFATYKRAHL-----FTDLERLSKLVNPNPVPQ 547
||| : : : : :
Qy 450 WLFVKFVSLVLFNKAFLVFGGVPKQYALIKADGIP-----IENY-----IARTMDGV 498
||| : : : : :
Db 548 FLFT-----GRAHPHDGAG-QGLIKRIVEISQRPEFLGKIIFLENYDMQLARRL--- 595
||| : : : : :
Qy 499 AENSHVRKQNYFYNYCLTGKFLRNCPTYLREAFAT-----LKSQVDNLTVSTNFMEE 554
||| : : : : :
Db 596 -----VTGQDIWLNTPTPLPEASGTSGEKALMNGVL-NFSVLGDGWLWG 638
||| : : : : :
Qy 555 LK-----ARTYTKVILMDHVDLMDMPVANLAECLAKQVAP-----GGI 593
||| : : : : :
Db 639 YREGAGWALTEKRYQN---OEHQDQLD-----AATYISILETEILPLYYARNKKGYSIGWI 692
||| : : : : :
Qy 594 VIMRS--ASLSPPYAELIQAGFDVRCIRRATQGYMDRVNNYSSFYMARRGAKK 646
||| : : : : :
Db 693 KSVKNSIAQIAPHYT-----MKRQLDDY-----YSKFYCKEAKRFXE 729
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US-11-079-463-7941
; Sequence 7941, Application US/11079463
; Publication No. US20060073161A1
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO BACTEROIDES FRAC
; FILE REFERENCE: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: PATH00-03DIV2
; CURRENT APPLICATION NUMBER: US/11/079,463
; CURRENT FILING DATE: 2005-03-14
; PRIOR APPLICATION NUMBER: US 60/128,705
; PRIOR FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: US 09/540,209
; PRIOR FILING DATE: 2000-04-04
; NUMBER OF SEQ ID NOS: 10444
; SEQ ID NO 7941
; LENGTH: 688
; TYPE: PRT
; ORGANISM: B.fragilis
US-11-079-463-7941

Query Match 2.9%; Score 101; DB 11; Length 688;
Best Local Similarity 19.0%; Pred. No. 1.1; Indels 154; Gaps 26;
Matches 84; Conservative 68; Mismatches 137;

Qy 187 LPL-LQMPWRRPF-----WRSIFDIDNI-----DIGPERRAYLEQKLERVW---- 227
||| : : : : :
Db 203 LPLDKHETWLRQWILEEHKEWR-----PNVYGCKSWLMDGLQPRV-VSRDLD--WGIPV 254
||| : : : : :
Qy 228 -EQNTQSQSIPYVPLRAPYVWIGRLPSVGHALHEERVERPMPPTFLYTQSWED--PE 284
||| : : : : :
Db 255 PVEGAEKGVLYV-WFDAP-----IGVISNTE-----LLPDSMETWTKD 292
||| : : : : :
Qy 285 PMEVMSEINPKDVTLTSTGGCNALNLLVQGAGQVVSVDNCPAQSA--LELKVAIQOLE 343
||| : : : : :
Db 293 PETRLVHIFIGKDNIVF-----HCIVFPAMLKAGSYIIPDNVPSNEFLNLEGDKIS----- 343
||| : : : : :
Qy 344 FEDVWQLFGEVHPRIEELYEKKLAPFLSOTSNFWSKRLWYFQHGLYQGGMGKLCWVL 403
||| : : : : :
Db 344 -----TSRN-WA--VWLHEVLEDFPKQDVLRYVL 370
||| : : : : :
Qy 404 QCLAVVLGLGKTVKRLANAPTMEEQRRLWDSNMLIHFVNGPKPLWLVFKV--SLVLF 461
||| : : : : :
Db 371 -----TANAPETKDNDEFTWKD-----FQARNNELVAVYGNFVNRAMVLT 410
||| : : : : :
Qy 462 NKAVLWFGGVGPG-----KOYALIKADGIPLENYVIARTMDGVAENSHVRKQNY 509
||| : : : : :
Db 411 QK-----YFEGKVPAAAGELTDYDKETLKEFSDVKAIEVEKLLN-VFKRDAQKAMMLAR--- 463
||| : : : : :
Qy 510 FYNYCLTGKFLRNCPTYL-----REAAFPATLKSQVVDNLTVSTNFMEEELKARTYTKV 563
||| : : : : :
Db 464 -----IGNKYLADTEPKWLAKTDMERVGTILNISLQLVANLAIAPPEPL-PPSSERLRQM 517
||| : : : : :
Qy 564 ILMDHVDLMD-----MPVANEL 580
||| : : : : :
Db 518 LNMDSFDAWELGRNDLLPAGHQL 540
||| : : : : :
US-11-188-298-13759
; Sequence 13759, Application US/11188298
; Publication No. US20060075522A1
; GENERAL INFORMATION:
; APPLICANT: Abad, Mark S. et al.
; TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
; FILE REFERENCE: 38-21(53452)B
; CURRENT APPLICATION NUMBER: US/11/188,298
; CURRENT FILING DATE: 2005-07-22
; PRIOR APPLICATION NUMBER: 60/592,978
; PRIOR FILING DATE: 2004-07-31
; NUMBER OF SEQ ID NOS: 22569
; SEQ ID NO 13759
; LENGTH: 549
; TYPE: PRT
; ORGANISM: ASPERGILLUS NIDULANS FGSC A4
US-11-188-298-13759

Query Match 2.9%; Score 99; DB 11; Length 549;

```
Best Local Similarity 20.0%; Pred. No. 1.2;
Matches 103, Conservative 66, Mismatches 177, Indels 170, Gaps 25;

Qy 207 DNIDIGERRAYLEOKL---BRVNEQNTQG--SIPYVPWLRAPIYVWIGRLPSVGHALHE 261
Db 58 DEIBIIFSKPLTUKMLAMSEKIREQFRAGLESSP-----INMLPSYNHAL-- 103
Qy 262 ERVERPMPFPFLYTQSWEDPEPDMVMEINPKDVTILTSGGCN---ALNLLVOGAG 317
Db 104 -----PTGL-----EGTFLALDVGGSTVRVALIELCGQGM 135
Qy 318 QVWSVDCNPAQSALLEKKVAIOOLEFEDVWQLFEGVHPRIEEL---YEKKLAPF--- 370
Db 136 EVLAV-----SSSLIDNVKLEGTSPFD-W--NAEKIEEMLREVGTNYGREEAPLSNGL 187
Qy 371 -----LSQTSNFWSKRLWYFQHGLYYQGGMKLC--WVLOCLAVL-----GLKGT 415
Db 188 SWSPPFIEQTS-----ISSGLVIHMGKFRCSMGTVGQELGSLIVOSQKRGLNVR 237
Qy 416 VKRLANAPTMEEQORLW-----DSNMLIHFV-----XNGPKPLVWLFVKF 455
Db 238 VDAIVNDSAAALLRAYVDPTTRNSLILGTGTVAIHPPVHAIGLGFGRKPOGNF--DY 295
Qy 456 VSLVLFNKAVLWFGGYPGKQYALIKADGPIENYIARTMDGVAENSHVRKQNYFYNNCL 515
Db 296 AKHVIINSEMSFGGV-----LPMTW-----DDILNRTHLRDPYQPLEYMA 338
Qy 516 TGKPLRD-----NCPYYIREAFAFATLKSQGVVDNLVTSTNFMEEB--- 554
Db 339 TGYLGEIVRLIIVDAVETAQLFGGELPHSMRDA--YSLDTSIVAFIEADTSPFLTASAA 396
Qy 555 --LKARTYTKVILMDHVDLMDPVAELAECLAKQVAPGGIVW-----RSAS 600
Db 397 LQKEHTWSRPPSPEDRULF--LRVCRISKRAAGYLATAHSMCLNREABISOGPPSPS 455
Qy 601 LSPPYAELIQXAGDVRCCRATQGYMDRVNMYSSF 636
Db 456 FKGRDVTVTSGNSDCLSIACDSGV--INKYPGF 489

RESULT 7
US-11-301-554-1903
; Sequence 1903, Application US/11301554
; Publication No. US20060088527A1
; GENERAL INFORMATION:
; APPLICANT: Henderson, Robert A.
; APPLICANT: Wang, Tongtong
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Kalos, Michael D.
; APPLICANT: Sleath, Paul R.
; APPLICANT: Johnson, Jeffrey C.
; APPLICANT: Retter, Marc W.
; APPLICANT: Durham, Margarita
; APPLICANT: Carter, Darick
; APPLICANT: Fager, Gary R.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Bangu, Chaitanya S.
; APPLICANT: McNabb, Andria
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE, 210121.478C21
; CURRENT APPLICATION NUMBER: US/11/301,554
; CURRENT FILING DATE: 2005-12-13
; PRIOR APPLICATION NUMBER: US 10/283,017
; PRIOR FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: US 10/113,872
; PRIOR FILING DATE: 2002-03-28
; PRIOR APPLICATION NUMBER: US 10/017,754
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: US 09/902,941
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: US 09/849,626
; PRIOR FILING DATE: 2001-05-03
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; PRIOR APPLICATION NUMBER: US 09/736,457
; PRIOR FILING DATE: 2000-12-13
; PRIOR APPLICATION NUMBER: US 09/702,705
; PRIOR FILING DATE: 2000-10-30
; PRIOR APPLICATION NUMBER: US 09/677,419
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: US 09/671,325
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US 09/658,824
; PRIOR FILING DATE: 2000-09-08
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 2157
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1903
; LENGTH: 2209
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-301-554-1903

Query Match 2.8%; Score 97; DB 10; Length 2209;
Best Local Similarity 19.9%; Pred. No. 14;
Matches 110; Conservative 76; Mismatches 226; Indels 140; Gaps 24;

Qy 94 LAKFK--SIYVVDLCHSLCEVAKKAKGKNVQVVEADACQFAPPEGTATLITFSYSL 151
Db 1626 LMKFSLDTLYVSTAKH---VFEEKLP---KLLKLTQAKSSTLINKETKITQTIESCL 1678
Qy 152 TMPPFHNVDQACSYLSQDGLGVADFYVG--KYDLPRLQMPHRSRFFWRSIFDIDNID 210
Db 1679 LSIYNPEWAVAIAS--LAQD--IPEGFKISALFKCLYLAER-----W-----LQNP 1723
Qy 211 IGPERRAYLEQKLERVMEQNTQGSIPYVWMLRAPYVWIGRLPSVGHALHEERVERPMPF 270
Db 1724 SQEKREKAKALLKLIHQYRSSTEAV-----LJAHKLNTEEYLR-VIG 1767
Qy 271 PPTFLYTQSWEDPEPDMVMEINPKOTVLTITSGGCNALLNLVQAGOVSVSDCNPAQSA 330
Db 1768 KPAHLIVSLYEHP-----SINQIQNSSGTDYPDIHAAAKE 1803
Qy 331 LLELKKVAIOOLEPEVDVWQLFGE-----GVHPRIEELYE-----KKLAPFLSQT 374
Db 1804 IAE-----VNEINLEKVDMDLLEKWLCPSTKPGKEP--SELFQEDALRRVQVLLLSR 1856
Qy 375 SHNFWSKRLWYFQHGYYQGGMKLCW-----VLQCLAVVLGLGKTVKRLANAPTEBQR 429
Db 1857 PIDYSSRMLFVFATSTTTILGMHQLTFAHRTALQCL-FYLADKETIESLFKKPIEEVKS 1915
Qy 430 RLWDSNMLIHF-----VKNQPKPLVW-----LFVKFVSLVLFNKAV-- 465
Db 1916 YLRCTITFLASFETLNIPIITVELFCSPKEGMKGLKWNHSHESMAVRLVTELCLKEYKIYD 1975
Qy 466 --LWFGGVPGKQYALIKADGPIENYIARTMDGVAENSHVRKQNYF---YNYCLTGKFL 520
Db 1976 LQLWNG-----LLOKLGLGFMNIPYLRKVLKAISSIHSLWQYFYSKAWQVRIQIPL 2027
Qy 521 RDNCP-----TYLREAAFATK---SGVVDNLVTSTNFFMEELKARTYTKVILMDHVDW 571
Db 2028 SASCPFLSPDQLSDCSSESLIAVLECPVSGDLDLIGVARQYIOLELPALACLMLMPHSEK 2087
Qy 572 LDMPEVANELAEC 583
Db 2088 RHQIQKNFLGSC 2099

RESULT 8
US-10-467-657-7224
; Sequence 7224, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
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; APPLICANT: MONACI Elisabetta
; FILE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: Seqmin99, version 1.04
; SEQ ID NO 7224
; LENGTH: 326
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-7224

Query Match          2.8%; Score 96; DB 9; Length 326;
Best Local Similarity 25.9%; Pred. No. 1.1;
Matches 30; Conservative 21; Mismatches 39; Indels 26; Gaps 6;

QY 120 KGKNVQVVEADACQFAPP---EGTATLITFSYSLTMIPPF-----HNV--IDQACS--- 166
DB 214 EGWLEHEVTRLTVCYLKPLADGIDTLVLGCTHFPFLKPLIGRAHNVALVDSAITTAE 273

QY 167 ----VLSQDLGVAD-----FYSGKYDLPLQMPHSRRFFWRSIFDIDNIDIG 212
DB 274 ETARVLAQGLDTCNNPNDRFYVS---DIPLKFTTIGERPLGRTMEQIEWVSIG 326

RESULT 9
US-11-115-639-31
; Sequence 31, Application US/11115639
; Publication No. US20050282242A1
; GENERAL INFORMATION:
; APPLICANT: Rothstein, David
; APPLICANT: Murphy, Christopher
; APPLICANT: MacNeil, Ian
; TITLE OF INVENTION: SCREENING ASSAYS FOR ANTIMICROBIAL
; TITLE OF INVENTION: AGENTS
; FILE REFERENCE: 50150/075003
; CURRENT FILING DATE: 2005-04-27
; PRIOR APPLICATION NUMBER: 60/566,858
; PRIOR FILING DATE: 2004-04-30
; PRIOR APPLICATION NUMBER: 60/565,679
; PRIOR FILING DATE: 2004-04-27
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 31
; LENGTH: 2890
; TYPE: PRT
; ORGANISM: H. pylori
US-11-115-639-31

Query Match          2.8%; Score 95.5; DB 11; Length 2890;
Best Local Similarity 18.9%; Pred. No. 28;
Matches 101; Conservative 82; Mismatches 150; Indels 201; Gaps 29;

QY 214 ERRAY-----LEOKLERVWE---QNTQGSIPYVPLRAPYVYVWIGRLPSVGHALH 260
DB 1775 EERGAYTTLKQAKRMIEQKSNEVWECLQEITEG-----YPLVLLNRAPT-----LH 1819
QY 261 EERVERPMPPTFLYTQSWEDEPDPMEVMEINP----- 294
DB 1820 QKSIQ---AFHPKLI-----DGKAIQLHPLVCSAFNADFQDQMAVHVPLSQEAI 1866
QY 295 -KDTVLTITSGGCNALNLLVQAGOVSVDCNPAQSALLELKVAIQOLEFEDVWOLFGE 353
DB 1867 AECKVLMSS-----MNLIPASGRAVAI---PSQDMVLGYLYLSLEKSGVKGHEKLFSS 1918
QY 354 -----GVHPRIEELYE-----KKLAPFLSQTSHNFWSKRLWYFQ 387
DB 1919 VNEIITAITDKELDIHAKIRVLDQGNIIATSAGRMIKSIILPDFIPT---DLWNRPMKKD 1976
QY 388 HG-----LYOQGMKGLCWVLOCL-----AVVLGLG-----KTVKRLANAPTWE 426
DB 1977 IGVLDVYVHKVGGIGITATFLDNLKTLGFRYATKAGISISMEDIITPKDKQKQVKEAKVE 2036
QY 427 EQR---RLWDSNMLHFVKNGPKPLVWLFV-----KFVSLVL-----FNKAVLWFGGVP 473
DB 2037 VKKIQQQYDQGLLTDOERYNKIIDTWTEVNDKMSKEMMTAQAQKEGNSIYMMADSGAR 2096

; APPLICANT: MONACI Elisabetta
; FILE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: Seqmin99, version 1.04
; SEQ ID NO 7224
; LENGTH: 326
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-7224

Query Match          2.8%; Score 96; DB 9; Length 326;
Best Local Similarity 25.9%; Pred. No. 1.1;
Matches 30; Conservative 21; Mismatches 39; Indels 26; Gaps 6;

QY 120 KGKNVQVVEADACQFAPP---EGTATLITFSYSLTMIPPF-----HNV--IDQACS--- 166
DB 214 EGWLEHEVTRLTVCYLKPLADGIDTLVLGCTHFPFLKPLIGRAHNVALVDSAITTAE 273

QY 167 ----VLSQDLGVAD-----FYSGKYDLPLQMPHSRRFFWRSIFDIDNIDIG 212
DB 274 ETARVLAQGLDTCNNPNDRFYVS---DIPLKFTTIGERPLGRTMEQIEWVSIG 326

RESULT 9
US-11-115-639-32
; Sequence 32, Application US/11115639
; Publication No. US20050282242A1
; GENERAL INFORMATION:
; APPLICANT: Rothstein, David
; APPLICANT: Murphy, Christopher
; APPLICANT: MacNeil, Ian
; TITLE OF INVENTION: SCREENING ASSAYS FOR ANTIMICROBIAL
; TITLE OF INVENTION: AGENTS
; FILE REFERENCE: 50150/075003
; CURRENT FILING DATE: 2005-04-27
; PRIOR APPLICATION NUMBER: 60/566,858
; PRIOR FILING DATE: 2004-04-30
; PRIOR APPLICATION NUMBER: 60/565,679
; PRIOR FILING DATE: 2004-04-27
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 32
; LENGTH: 2890
; TYPE: PRT
; ORGANISM: H. pylori
US-11-115-639-32

Query Match          2.8%; Score 95.5; DB 11; Length 2890;
Best Local Similarity 18.9%; Pred. No. 28;
Matches 101; Conservative 82; Mismatches 150; Indels 201; Gaps 29;

QY 214 ERRAY-----LEOKLERVWE---QNTQGSIPYVPLRAPYVYVWIGRLPSVGHALH 260
DB 1775 EERGAYTTLKQAKRMIEQKSNEVWECLQEITEG-----YPLVLLNRAPT-----LH 1819
QY 261 EERVERPMPPTFLYTQSWEDEPDPMEVMEINP----- 294
DB 1820 QKSIQ---AFHPKLI-----DGKAIQLHPLVCSAFNADFQDQMAVHVPLSQEAI 1866
QY 295 -KDTVLTITSGGCNALNLLVQAGOVSVDCNPAQSALLELKVAIQOLEFEDVWOLFGE 353
DB 1867 AECKVLMSS-----MNLIPASGRAVAI---PSQDMVLGYLYLSLEKSGVKGHEKLFSS 1918
QY 354 -----GVHPRIEELYE-----KKLAPFLSQTSHNFWSKRLWYFQ 387
DB 1919 VNEIITAITDKELDIHAKIRVLDQGNIIATSAGRMIKSIILPDFIPT---DLWNRPMKKD 1976
QY 388 HG-----LYOQGMKGLCWVLOCL-----AVVLGLG-----KTVKRLANAPTWE 426
DB 1977 IGVLDVYVHKVGGIGITATFLDNLKTLGFRYATKAGISISMEDIITPKDKQKQVKEAKVE 2036
QY 427 EQR---RLWDSNMLHFVKNGPKPLVWLFV-----KFVSLVL-----FNKAVLWFGGVP 473
DB 2037 VKKIQQQYDQGLLTDOERYNKIIDTWTEVNDKMSKEMMTAQAQKEGNSIYMMADSGAR 2096
```

QY 474 GK-----QYALIKADGPIENYIARTMDGVAENSHVRKQNYFYNNCLTG--KELR 521
Db 2097 GSAQIROLSAMRGLMTKPDGSIITPTI---ISNFKEGNLVLE-----YFNSTHGARKGLA 2149
QY 522 DNCPTYLREAAAFATLKSGVWNLTVSTNF-----FMBELKAR 558
Db 2150 D---TALKTANAGYLTRKLD---VSQNVKVVSDCGTHEGIEITDIAVGSELIEPLEER 2203
QY 559 TYTKVILMDHVDLMPVANEL---AECL-----AKQVAPGGIVIVRSASLSPP 604
Db 2204 IFGRVLLEDVID---PITNEILLYADTLIDEGAKKVVVEAGI---KSITITRTP 2250
RESULT 11
US-11-115-639-33
; Sequence 33, Application US/11115639
; Publication No. US20050282242A1
; GENERAL INFORMATION:
; APPLICANT: Rothstein, David
; APPLICANT: Murphy, Christopher
; APPLICANT: MacNeill, Ian
; TITLE OF INVENTION: SCREENING ASSAYS FOR ANTIMICROBIAL
; TITLE OF INVENTION: AGENTS
; FILE REFERENCE: 50150/075003
; CURRENT APPLICATION NUMBER: US/11/115,639
; CURRENT FILING DATE: 2005-04-27
; PRIOR APPLICATION NUMBER: 60/566,858
; PRIOR FILING DATE: 2004-04-30
; PRIOR APPLICATION NUMBER: 60/565,679
; PRIOR FILING DATE: 2004-04-27
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 33
; LENGTH: 2890
; TYPE: PRT
; ORGANISM: H. pylori
US-11-115-639-33

Query Match 2.8%; Score 95.5; DB 11; Length 2890;
Best Local Similarity 18.9%; Pred. No. 28;
Matches 101; Conservative 82; Mismatches 150; Indels 201; Gaps 29;
QY 214 ERRV-----LEOKLERVWE---ONTQGSIPYVPLRAPYVYVIGRLPSVGHALH 260
Db 1775 EERGATTLKQAKRMIEQKSNEVWECLOETEG-----YPVLINRAPT-----LH 1819
QY 261 EERVPRPMPFPPTFLYTQSWEDPEPDMVEINP-----DGKAIQLHPLVCSAFNADFDGDMVHVPLSQEAI 1866
Db 1820 KQSIQ---AHPKLI-----DKRAIQLHPLVCSAFNADFDGDMVHVPLSQEAI 1866
QY 295 -KDTVLTTSGGCNALNLVQAGQVSDCNPAQSALLELKVAIQOLEFEDVWQLFGE 353
Db 1867 AECKVLMSS-----MNLIPASGRAVAI---PSQDMVLGLYLSLEKSGVKGEHKLFS 1918
QY 354 -----GVHPRIEELYE-----KKLAPFLSOTSHNFWSKELWYFQ 387
Db 1919 VNEIITAIDTKELDIHAKIRVLDQGNIIATSGRMIKSIILPDFIPT---DLWNRPMKKD 1976
QY 388 HG-----LYYQCGMGKLCWLQCL-----AVVLGLG-----KTVKRLNAPATME 426
Db 1977 IGLVDYVHKVGIGITATFLDLNLKTLGFRYATKAGISMEDIIITPKDKQKMEKARVE 2036
QY 427 EQR---RLNDSNMLIHFKVNGPKPLVWLFV-----KFSVLV-----FNKAVLWFGGVP 473
Db 2037 VKKIQOQYDQGLITDQERYNKIIDTWTVEVNDKMSKEMMTAIAQDKEGFNSIYMADSGAR 2096
QY 474 GK-----QYALIKADGPIENYIARTMDGVAENSHVRKQNYFYNNCLTG--KELR 521
Db 2097 GSAQIROLSAMRGLMTKPDGSIITPTI---ISNFKEGNLVLE-----YFNSTHGARKGLA 2149
QY 522 DNCPTYLREAAAFATLKSGVWNLTVSTNF-----FMBELKAR 558

Db 2150 D---TALKTANAGYLTRKLD---VSQNVKVVSDCGTHEGIEITDIAVGSELIEPLEER 2203
QY 559 TYTKVILMDHVDLMPVANEL---AECL-----AKQVAPGGIVIVRSASLSPP 604
Db 2204 IFGRVLLEDVID---PITNEILLYADTLIDEGAKKVVVEAGI---KSITITRTP 2250
RESULT 12
US-11-096-568A-2582
; Sequence 2582, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nickolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; TITLE OF INVENTION: Therapy
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 2582
; LENGTH: 658
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; NAME/KEY: misc feature
; LOCATION: (1)-(658)
; OTHER INFORMATION: Ceres Seq. ID no. 15176030
US-11-096-568A-2582

Query Match 2.7%; Score 94; DB 11; Length 658;
Best Local Similarity 19.6%; Pred. No. 4.5;
Matches 115; Conservative 69; Mismatches 182; Indels 220; Gaps 30;
QY 20 EKLKLSMKDGLTVLRHMWFGSKGD-----DHAARLESFYGPAAAPARLAER 69
Db 56 EKLQLAGVSQRCVVL-----GSSKAEDKHLQLVHTKQHVNLVKSISTKQDYRRNRIASQ 110
QY 70 SNLIWVDLGGGTGENVDMMADYIDLAKFKSIYVVDLHSLCEVAKKAKAKGKNVQVVE 129
Db 111 LNSIY--LNGGSEAAVLAAG-----SVVKLAEKVABG-----E 142
QY 130 ADACQFAPPEGTATLITFSYSLTMIPPHNVIDQACSYLSQDGLGVADFYVSGKYDLP 189
Db 143 LD-CGFA-----IVRPPGHAEADAMGFCLENNVAVAAASFLTNERPDLGV 187
QY 190 RQ---MPW-----SRRFFWRS---IFDINDIDIGERRAYLEOKLERVWEQNTQGS 235
Db 188 KKILIVDWDVHHNGTQKMFWKDPRVLFFSVHRHEYGGFYAGDDGYNMVMYGEQGEF 247
QY 236 PYVPWLRAPYVYVWIGRLPSVGHALHEERVERPPM--PPPTFLYTQSWEDPEPD----- 286
Db 248 INVWDQ-----GRCGDADYLAANDHILLIPVAREFNPVIFLSAGFDAINDPLGGCC 300
QY 287 -----MEVMEINPKDTVLTITSGGCNALNLVQAGQVSDCNPAQSALLELK 336
Db 301 VTPYGSVMLKKLMEFAQGGKIVLAL-EGGYN-LDSIAKSSLACVQV-----LLEDKQ 350
QY 337 V--AIQOLEFEDVWQLFGEVHPRI-----BEL-----YEKLAFFL-----SOTS 375
Db 351 IQGPPEAYPFPESTWRVI--QAVRKELCTYWPSLADELSWKLINQKTPTPTIILISSDSE 409
QY 376 HN-----FWSKRL-----WYFOHG-----L 390
Db 410 DNAOGLLDQMSKLSIENPOGTILLENHVEPASTSWRADLAKVDVWYASFGSNMMPKFLC 469
QY 391 YYQGMGKLCWVLOCLAVVLGLGKTVKRLANAPTWMEBORLWDSNMLIHFKVNGPKPLW 450
Db 470 YIQGGQ-----VDGLKKVC-----VGSMD-----KSPPKETVM 497
QY 451 LFVFEVSLVLFNK--AVLWFGGYPGKOYALIKADGPIENYIART 494
Db 498 --ETFPHRLFFRGRESSVGMVGGV-----AFTNPLANLIDQT 532

RESULT 13

US-11-096-568A-2581
; Sequence 2581, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nickolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; TITLE OF INVENTION: Theby
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 2581
; LENGTH: 660
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(660)
; OTHER INFORMATION: Ceres Seq. ID no. 15176029
; US-11-096-568A-2581

Query Match 2.7%; Score 94; DB 11; Length 660;
Best Local Similarity 19.6%; Pred. No. 4.5;
Matches 115; Conservative 69; Mismatches 182; Indels 220; Gaps 30;

Qy 20 EKLKSSMKDDTLVLRHWMFGSKGD-----DHAARLESFYGPQAFAARLAER 69
 |||: : |||: : |||: : |||: : |||: : |||: : |||: : |||: :
Db 58 EKLQAGVSQRVVVL-----GSSKAEDKHLQLVHTKDHNLVKSISTKQDYRNRITASQ 112
 |||: : |||: : |||: : |||: : |||: : |||: : |||: : |||: :
Qy 70 SNLIWDLGGGTGENVDMMADYIDLAKFSIYVDLCHSLCEVAKKAKAKGNKVQVE 129
 |||: : |||: : |||: : |||: : |||: : |||: : |||: : |||: :
Db 113 LNSIY--LNGSSSEAAYLAAG-----SVVKLEAKVAEG-----E 144
 |||: : |||: : |||: : |||: : |||: : |||: : |||: : |||: :
Qy 130 ADACQFAPPEGTATLTIFSYSLTMIPPPHNVIDACS YLSQDGLGVGADFVSGKYDIPL 189
 |||: : |||: : |||: : |||: : |||: : |||: : |||: : |||: :
Db 145 LD-CGFA-----IVRPGGHAADEANMGECFLNNVAVASFLINERPDLGV 189
 |||: : |||: : |||: : |||: : |||: : |||: : |||: : |||: :
Qy 190 RQ---MPW-----SRFFWR-----IFDINDIGERRAYLEQKLERVWEQNTGSI 235
 |||: : |||: : |||: : |||: : |||: : |||: : |||: : |||: :
Db 190 KXILIVDWVHHGNGTQMFKWDPRVLFFSVHRHEYGFYPAGDDGYNMVGEGPGEGFN 249
 |||: : |||: : |||: : |||: : |||: : |||: : |||: : |||: :
Qy 236 PYVPWLRAPIYYVMGRGPSVCHALHEERVERPPM--FPPTFLYTQSWEDEPED----- 286
 |||: : |||: : |||: : |||: : |||: : |||: : |||: : |||: :
Db 250 INVPDQ-----GRCGDADYLAAWHILIPVAREFPNDVIFLSAGFDAINDPLGCC 302
 |||: : |||: : |||: : |||: : |||: : |||: : |||: : |||: :
Qy 287 -----MEVMENPKDTVLTLTSGCNALNLLVQGAGOVVSDCNPAQSALLELK 336
 |||: : |||: : |||: : |||: : |||: : |||: : |||: : |||: :
Db 303 VTPYGYSVMLKKLMFAQGIKVLAL-EGYN-LDSIAKSSLACQV-----LLEDKQ 352
 |||: : |||: : |||: : |||: : |||: : |||: : |||: : |||: :
Qy 337 V-AIQLEFEDVMQLFGEGVHPRI-----BEL-----YEKKLAPFL-----SOTS 375
 |||: : |||: : |||: : |||: : |||: : |||: : |||: : |||: :
Db 353 IQGPPEAYPFESTWRVI-QAVRKELCTYWPSSLADELSWKLINOKTPTPIILISSDSETE 411
 |||: : |||: : |||: : |||: : |||: : |||: : |||: : |||: :
Qy 376 HN-----FWSKEL-----WFQHG-----L 390
 |||: : |||: : |||: : |||: : |||: : |||: : |||: : |||: :
Db 412 DNAOGLLDQMSKLSIENPQGTLLNHQVEPASTSWRADLAKVDVWYASFSGSNMWKPRLC 471
 |||: : |||: : |||: : |||: : |||: : |||: : |||: : |||: :
Qy 391 YYQGMGKCLWLOCLAVLGLGKTVRKRLANAPTWEORRLWDSNMLTIHFVKGNGPKPLVW 450
 |||: : |||: : |||: : |||: : |||: : |||: : |||: : |||: :
Db 472 YIQGGQ-----VDGLKKVC-----VGSMD-----KSPFKVTW 499
 |||: : |||: : |||: : |||: : |||: : |||: : |||: : |||: :
Qy 451 LFVKFVSLVLPNK--AVLWFGGGVPGQGYALIKADGPIENWIART 494
 |||: : |||: : |||: : |||: : |||: : |||: : |||: : |||: :
Db 500 --BTFFPHRLFfGRESSVWGwGGV-----AFTNPPLANLIDOT 534
 |||: : |||: : |||: : |||: : |||: : |||: : |||: : |||: :

; APPLICANT: Alexandrov, Nickolai et al.
 ; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
 ; TITLE OF INVENTION: Theby
 ; FILE REFERENCE: 2750-1592PUS2
 ; CURRENT APPLICATION NUMBER: US/11/096,568A
 ; CURRENT FILING DATE: 2005-04-01
 ; NUMBER OF SEQ ID NOS: 34471
 ; SEQ ID NO 2580
 ; LENGTH: 680
 ; TYPE: PRT
 ; ORGANISM: Arabidopsis thaliana
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; LOCATION: (1)..(680)
 ; OTHER INFORMATION: Ceres Seq. ID no. 15176028
 US-11-096-568A-2580

Query Match 2.7%; Score 94; DB 11; Length 680;
 Best Local Similarity 19.6%; Pred.No.4.7;
 Matches 115; Conservative 69; Mismatches 182; Indels 220; Gaps 30;

Qy	20	EKLSSMKDILTVRHWMFGSKGD-----DHAARLESFYGPQAAAPAAALAE	69
Db	78	EKLQAGVQRVVL-----GSSKAEDHQLVHTKDHVNLVKSISTKQDYRNRIASQ	132
Qy	70	SNLIWVDLGGGTGENVDMMADYIDIAKFSIYVVDLCHSLCEVAKKAKAKGKNVQVVE	129
Db	133	LNSIV--LNGSSEAAVLAAG-----SVVKLAEKVAG-----E	164
Qy	130	ADACQAPPGETATLITFSYSLTWIPPHNVIDQACSVLSQDLGVGVAIFYSGKYDLPL	189
Db	165	LD-CGFA-----IVRPPGHAEADAMGFLFNNAVVAASFLLNERPDLGV	209
Qy	190	RO---MPW-----SRRFWR-----IFDIDNIDIGPERRAYLEQKLRVWEQNTQGS	235
Db	210	KKILIVDWDVHNGTQKMFWDPRVLF9VHRHEYGGFYAGDDGDYNNVGECPGEGFN	269
Qy	236	PYPWLRAPYYVWIGRLPSVGHALHEERVHPPM--FPPTFLYTOSWEDPEPD-----	286
Db	270	INVPDQ-----GRCGDADYLAADWHILIPVAREFNPDIFLSAGFDAINDPLGGCC	322
Qy	287	-----MEVMEINPKDTVLTITSGGCHALNLLVQAGQVVSVDGNPAQSALLEKK	336
Db	323	VTPGYSVMLKLMFEAGQKIVLAL-EGYN-LDSIAKSSACVQV-----LLEDKQ	372
Qy	337	V--AIQLEPEDVMOLFGEVHPRI-----BEL-----YEKKLAPFL-----SOTS	375
Db	373	IQGPPEAYPPESTWRVI--QAVRKRLCTVWPSLADELSWKLINQKTPPTLILSSDSETE	431
Qy	376	HN-----FWSKRL-----WYFHQ-----L	390
Db	432	DNAQGLLDQMSKLSIENPQGTLLNHHQVEPASTSWRADLAKVDVWVYASFGSNMWPFLC	491
Qy	391	YYQGMGKLCWVLOCLAVVLGLGKTVKRLANAPTWBEQRRLWDSNMLIHVKNQPKPLVW	450
Db	492	YIQGGQ-----VDGLKKVC-----VGSMD-----KSPPKETVW	519
Qy	451	LFVKFVSLVLPNK--AVLWFCGGVPGKOYALIKADGIPLENYIART	494
Db	520	--ETFPHRLPFGRESSVGVWGGV-----AFTNPLANLIDOT	554

RESULT 15
 US-11-153-185-7
 ; Sequence 7, Application US/11153185
 ; Publication No. US20060084796A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Alexandrov, Nickolai
 ; APPLICANT: Brover, Vyacheslav
 ; APPLICANT: Feldmann, Kenneth
 ; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA ENCODING
 ; TITLE OF INVENTION: METHYLTRANSFERASES
 ; FILE REFERENCE: 11696/175X01

RESULT 14
US-11-096-568A-2580
; Sequence 2580, Application US/11096568A
; Publication No. US20060048240A1
GENERAL INFORMATION:
; AFFILIANT: ALEXANDROV, NIKOLAI
; APPLICANT: Brover, Vyacheslav
; APPLICANT: Feldmann, Kenneth
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA ENCODING
; TITLE OF INVENTION: METHYLTRANSFERASES
; FILE REFERENCE: 11696/175X01

Search completed: May 5, 2006, 07:49:29
Job time : 48 secs


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Db 7 TTGATTACTTTTCGTATTTCATGTCGATGATCCCACTTTCATGCTGCTATCGATAT 66
Qy 164 AlaCysSerTyrLeuSerGlnAspGlyLeuValGlyValAlaAspPheTyrValSer--- 182
Db 67 GCTGTTTCTAAATTAGATATGGAAGGTATTATTGCCACTGTAGATTTTGGTATTCAAAGC 126
Qy 183 -----GlyTyrAsp-----LeuProLeuArgGlnMetPro 193
Db 127 AGTGACACCTCAATGGGTGCTATTAAATACTGTGTGGTGGTTGTTAAACAGGACATTCT 186
Qy 194 TrpSerArgGlnPhePheTyrArgSerIlePheAspIleAspAsnIleAspIleGlyPro 213
Db 187 TGGATATTACGTAATTTTGGAGATTTGGTTGAGCTGATAAAGTGTTTTGGATTCT 246
Qy 214 GluArgAlaIleTyrLeuGluGlnLysLeuGluArgValTrpGluGlnAsnThrGln--- 232
Db 247 TCAGAAGAAACTATTTCGAATATAAATTGGTACCGTCAAAATCTTTGAAATTCATACAAC 306
Qy 233 -----GlySerIleProTyrValProTrpLeuArgAlaProTyrTyrValTrpIle 249
Db 307 AAGGCTTTGGGTAAATC-----CCCTATTATATTGGGATT 342
Qy 250 GlyArgLeuProSerValGlyHisAlaLeuHisGluGlu-----ArgValGlu 265
Db 343 GGTGTGTATAATCAAAATCACACACCATTTTAGAAGATTGAATTTGTTAGCCACTGAA 402
Qy 266 ArgProProMetPheProThr----- 273
Db 403 TCCCTTACCTTGCTCCAACTACAACCTCAACTCGCTAATCAACTTGAAGATATTCCAATT 462
Qy 273 ----- 273
Db 463 TCTAAGTCAATGAAGCTGCTTTAATCAACTTGCAAAAAAATTTACCTTACCCATCAATG 522
Qy 273 ----- 273
Db 523 TACTATCAAAAAGGAATATTGGAGAGTCTACTATGATGAATGAATCCATTGTATGAACAA 582
Qy 274 -----PheLeuTyrThrGlnSerTrpGluAspProGluProAspMetGluVal 289
Db 583 TTTAAAAACCAATACATATTATGCTTTTCACTTGGGAAGATCCTCGTGAAGATCATAAACTT 642
Qy 290 MetGluIleAsnProLysAspThrValLeuThrLeuThrSerGlyGlyCysAsnAlaLeu 309
Db 643 TTGAATTTTACAGTGATGACTGTTTGGCTATTACTTCAGCTGGTGATAAATTTTG 702
Qy 310 AsnLeu-----LeuValGlnGlyAlaGlyGlnValValSerValAspCysAsnProAla 327
Db 703 AGTTATGCTAGTTTACCAACACCACCAAAAGATTTCATGCTGTTGATCTTAATCCATGT 762
Qy 328 GlnSerAlaLeuLeuGluLeuLysLysValAlaIleGlnGlnLeuGluPheGluAspVal 347
Db 763 CAAACCACTTTATTAGAATTTGAAATTTGGCTAGTTTGTAGATGCTTTCTCAAGAACAAAT 822
Qy 348 TrpGlnLeuPheGlyGluGlyValHisProArgIleGluGluLeuTyrGluLysLysLeu 367
Db 823 TGGTCAATGTTTGGTGAAGGTAAATTCGAAATTTCAATGATGCTTTTGATTGATACTTTG 882
Qy 368 AlaProPheLeuSerGlnThrSerHisAsnPheTrpSerLysArgLeuTriPtyrPheGln 387
Db 883 GCGCGCACATGCTCTTCTAATGCC-----TTCCAA 912
Qy 388 His 388
Db 913 CAC 915
```

RESULT 2

```
US-09-248-796A-12232
; Sequence 12232, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
```

```
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 12232
; LENGTH: 666
; TYPE: DNA
; ORGANISM: Candida albicans
US-09-248-796A-12232

Alignment Scores:
Pred. No.: 2,74e-09 Length: 666
Score: 158.00 Matches: 34
Percent Similarity: 55.7% Conservative: 20
Best Local Similarity: 35.1% Mismatches: 19
Query Match: 4.6% Indels: 24
DB: 3 Gaps: 3

US-10-620-914-45 (1-648) x US-09-248-796A-12232 (1-666)

Qy 51 LeuGluSerPheTyrGlyProGlnAlaAlaAlaPhe----- 62
Db 367 TTAGATGTCATTTCTAAGAATCAAGCTCATATTTATGATATAACACTAGAGAATTTTGTG 426
Qy 63 -----AlaAlaArgLeuAlaGluArgSerAsnLeu 72
Db 427 AAAGTAGACAAGATGCTCTTAGATTAGCTATTTCCCATTTTACCCAAAAGAAAGATCTT 486
Qy 73 IleTrpValAspLeuGlyGlyThrGlyGluAsnValAspMetAlaAspTyrIle 92
Db 487 ATTTGGATAGATATTGGTGGTGGAACTGGTTCCAATATTGAATTCATGATGAAATTAGT 546
Qy 93 AspleuAlaLys---PheLysSerIleTyrValValAspLeuCysHisSerLeuCysGlu 111
Db 547 AAAATATCTGAAACTTTTAAAGCTGTTTATTGGTTGATCTTCCCATCTTTTGTGTGAA 606
Qy 112 ValAlaLysLysAlaLysAla-----LysGlyTriPlys 123
Db 607 GTTGCTAAGGCAAGATTGGAATCCATGATTGACACACGGGACTGGAAA 657

RESULT 3
US-09-902-540-984/c
; Sequence 984, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(115849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 984
; LENGTH: 8832
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-902-540-984

Alignment Scores:
Pred. No.: 6,27e-05 Length: 8832
Score: 138.50 Matches: 97
Percent Similarity: 37.7% Conservative: 50
Best Local Similarity: 24.9% Mismatches: 138
```

```
Query Match: 4.0% Indels: 107
DB: 3 Gaps: 17
US-10-620-914-45 (1-648) x US-09-902-540-984 (1-8832)

QY 252 LeuProSerValGlyHisAlaLeuHisGluGluArgValGluArgProProMetPhePro 271
DB GTTCGAGGTAGAACCATGCCATGAACCTGGCCCTGGTTTCAGCCGCCCTT----- 2288
QY 272 ProThrPheLeuTyrThrGlnSerTrpGluAspProGluProAspMetGluValMetGlu 291
DB ---CCCTTGAAGTTCCCGCTTCCGGGAGGATCCGCGCTGGAGTTGGCGCTCGTCGAG 2231
QY 292 IleAsnProLysAspThrValLeuThrLeuThrSerGlyCysAsnAlaLeuAsnLeu 311
DB GTTCGAGGTAGAACCATGCCATGAACCTGGCCCTGGTTTCAGCCGCCCTT----- 2288
QY 312 LeuValGln---GlyAlaGlyGlnValSerValAspCysAsnProAlaGlnSerAla 330
DB GTTCGAGGTAGAACCATGCCATGAACCTGGCCCTGGTTTCAGCCGCCCTT----- 2288
QY 331 LeuLeuGluLeuLysValAlaIleGlnGlnLeu-----Glu 343
DB GTTCGAGGTAGAACCATGCCATGAACCTGGCCCTGGTTTCAGCCGCCCTT----- 2288
QY 344 PheGluAspValTrpGlnLeu-----PheGlyGluGlyValHisProArg 358
DB GTTCGAGGTAGAACCATGCCATGAACCTGGCCCTGGTTTCAGCCGCCCTT----- 2288
QY 359 IleGluGluLeuTyrGlyLysLysLeuAlaProPheLeuSerGlnThrSerHis-AsnPh 378
DB GTTCGAGGTAGAACCATGCCATGAACCTGGCCCTGGTTTCAGCCGCCCTT----- 2288
QY 378 eTrpSerLysArg-LeuTrpTyrPheGlnHisGlyLeuTyrTyrGlnGlyMetGlyL 398
DB GTTCGAGGTAGAACCATGCCATGAACCTGGCCCTGGTTTCAGCCGCCCTT----- 2288
QY 398 ysLeuCysTrpValLeuGlnCysLeuAlaValLeuLeuGlyLysThrValLysA 418
DB GTTCGAGGTAGAACCATGCCATGAACCTGGCCCTGGTTTCAGCCGCCCTT----- 2288
QY 418 rgLeuAlaAsnAlaProThrMetGluGluGlnArgArgLeuTrpAspSerAsnMetLeu 438
DB GTTCGAGGTAGAACCATGCCATGAACCTGGCCCTGGTTTCAGCCGCCCTT----- 2288
QY 438 leHisPheValLysAsnGlyProLysProLeuValTrpLeuPheValLysPheValSerL 458
DB GTTCGAGGTAGAACCATGCCATGAACCTGGCCCTGGTTTCAGCCGCCCTT----- 2288
QY 458 euValLeuPheAsnLysAlaValLeuTrpPheGly-----GlyGlyValProGlyLysG 476
DB GTTCGAGGTAGAACCATGCCATGAACCTGGCCCTGGTTTCAGCCGCCCTT----- 2288
QY 476 lnTyrAlaLeuLysAlaAspGlyIleProIleGluAsnTyrIleAlaargThrMeta 496
DB GTTCGAGGTAGAACCATGCCATGAACCTGGCCCTGGTTTCAGCCGCCCTT----- 2288
QY 496 spGlyValAlaGluAsnSerHisValArgLysGlnAsnTyrPheTyrTyrAsnCysLeu 516
DB GTTCGAGGTAGAACCATGCCATGAACCTGGCCCTGGTTTCAGCCGCCCTT----- 2288
QY 516 hrdLysPheLeuArgAspAsnCysProThrTyrLeuArg---GluAlaAlaPheAla- 534
DB GTTCGAGGTAGAACCATGCCATGAACCTGGCCCTGGTTTCAGCCGCCCTT----- 2288
QY 535 --ThrLeuLysSerGlyValValAspAsnLeuThrValSerThrAsnPhePheMetGluG 554
DB GTTCGAGGTAGAACCATGCCATGAACCTGGCCCTGGTTTCAGCCGCCCTT----- 2288
QY 554 luLeuLysAlaArgThrTyrThrLysValIleLeuMetAspHisVal---AspTrpLeuA 573
DB GTTCGAGGTAGAACCATGCCATGAACCTGGCCCTGGTTTCAGCCGCCCTT----- 2288
QY 573 eufTyrTyrGlnGlyGlyMetGlyLysLeuCysTrpValLeuGlnCysLeuAlaValVal 610
DB GTTCGAGGTAGAACCATGCCATGAACCTGGCCCTGGTTTCAGCCGCCCTT----- 2288

QY 573 spMetProValAlaAsnGluLeuAlaGluCysLeuAlaLysGlnValAlaProGlyGlyI 593
DB AAGACGCGCTGTGGCGAGTGGGGCGGGTCTCGCACGTGAGCGCGCGCGCTTGGC 1492
QY 593 leValIleTrpArg-Ser-----AlaSerLeuSerProPro 604
DB CGTCCTCATCGCCAGCTCAACACCGCGGGACCTTCGGCGGCTTCTTCAGCCGCCCT 1432
QY 605 TyrAlaGluLeuIleGlnLysAla 612
DB TCGAGTTTCGATGACGCGCTCGCG 1408

RESULT 4
US-09-902-540-9203
; Sequence 9203, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 9203
; LENGTH: 990
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-902-540-9203

Alignment Scores:
Pred. No.: 4,18e-05 Length: 990
Score: 126.50 Matches: 94
Percent Similarity: 37.6% Conservative: 48
Best Local Similarity: 24.9% Mismatches: 131
Query Match: 3.7% Indels: 107
DB: 3 Gaps: 17

US-10-620-914-45 (1-648) x US-09-902-540-9203 (1-990)

QY 264 ValGluArgProProMetPheProThrPheLeuTyrThrGlnSerTrpGluAspPro 283
DB GTTCGAGGTAGAACCATGCCATGAACCTGGCCCTGGTTTCAGCCGCCCTT----- 2288
QY 284 GluProAspMetGluValMetGluIleAsnProLysAspThrValLeuThrSer 303
DB GTTCGAGGTAGAACCATGCCATGAACCTGGCCCTGGTTTCAGCCGCCCTT----- 2288
QY 304 GlyGlyCysAsnAlaLeuAsnLeuValGln---GlyAlaGlyGlnValValSerVal 322
DB GTTCGAGGTAGAACCATGCCATGAACCTGGCCCTGGTTTCAGCCGCCCTT----- 2288
QY 323 AspCysAsnProAlaGlnSerAlaLeuLeuLeuLysLysValAlaIleGlnLeu 342
DB GTTCGAGGTAGAACCATGCCATGAACCTGGCCCTGGTTTCAGCCGCCCTT----- 2288
QY 343 -----GluPheGluAspValTrpGlnLeu----- 350
DB GTTCGAGGTAGAACCATGCCATGAACCTGGCCCTGGTTTCAGCCGCCCTT----- 2288
QY 351 PheGlyGluGlyValHisProArgIleGluGluLeuTyrGluLysLeuAlaProPhe 370
DB GTTCGAGGTAGAACCATGCCATGAACCTGGCCCTGGTTTCAGCCGCCCTT----- 2288
QY 371 LeuSerGlnThrSerHis-AsnPheTrpSerLysArg-LeuTrpTyrPheGlnHisGlyL 390
DB GTTCGAGGTAGAACCATGCCATGAACCTGGCCCTGGTTTCAGCCGCCCTT----- 2288
QY 390 eufTyrTyrGlnGlyGlyMetGlyLysLeuCysTrpValLeuGlnCysLeuAlaValVal 410
```


; APPLICANT: Fanger, Gary
; APPLICANT: Retter, Mark
; APPLICANT: Solk, John
; APPLICANT: Day, Craig
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; FILE REFERENCE: 210121.427C9
; CURRENT APPLICATION NUMBER: US/09/439,313
; NUMBER OF SEQ ID NOS: 575
; CURRENT FILING DATE: 1999-11-12
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 373
; LENGTH: 1155
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-439-313-373

Alignment Scores:
Pred. No.: 0.000529 Length: 1155
Score: 118.50 Matches: 66
Percent Similarity: 37.4% Conservative: 19
Best Local Similarity: 29.1% Mismatches: 81
Query Match: 3.4% Indels: 61
DB: 3 Gaps: 11

US-10-620-914-45 (1-648) x US-09-439-313-373 (1-1155)

```
Qy 187 LeuProLeuArgGlnMetProTrrP-----SerArgArgPhePheTrpArgSerilePhe 204
Db 204 CTTCCCTGCTCCAGGGGAGTGGCAAGACGCTGGCGCTTCTGGAGA----- 254
Qy 205 AspIleAspAenIleAspIleGlyProGluArgAlaTyrLeuGluGlnLysLeuGlu 224
Db 255 -----CCAGCAGCAGCTCTGTAT-----GAA 275
Qy 225 ArgValTrpGluGlnAsnThrGlnGlySerileProTyrValProTrrPLeuArgAlaPro 244
Db 276 GACACTAGGAACAAGATGGGCAAGTGTGTCCCTGCTGCGAGGGGAG 335
Qy 245 TyrTyrValTrpIleGlyArgLeuProSerValGly---HisAlaLeuHisGluGluArg 263
Db 336 CGGCAAGACCAAGTGGCGCTTGGGAGACTACGATGACAGTGCCTTCATGGAGCCAG 395
Qy 264 ValGluArgProProMetPheProProThrPheLeuTyrThrGlnSerTrp-GluAsp-- 282
Db 396 GTACCACGTCCG-----TGGAGAAGATCT 419
Qy 283 -----ProGluProAspMetGluValMe 290
Db 420 GGACAAGCTCCACAGAGCTGCTGGTGGGTAAAGTCCCAAGAGGATCTCATGTCAT 479
Qy 290 t-----GluIleAsnProLysAsp-----ThrValLeuThrLeuTh 302
Db 480 GCTCAGGACACTGACGTGAACAAGAGGAGGACTGCTCTACATCTGCC 539
Qy 302 rSer-----GlyGlyCysAsnAlaLeuAsnLeuValGlnGlyAlaGlyGlnValVa 320
Db 540 CTCTGCCAATGGGAATTGAGAAGTAGTAAACTCTCTGCTGGACAGCAGATGCAACTTAA 599
Qy 320 lSerValAspCysAsnProAlaGlnSerAlaLeuLeuGluLeuLysLysValAlaIleGl 340
Db 600 TGTCTTGTAC---AACAAAAAGAGGAGCAGCTCTGATAAAG-----GCCGTACA 644
Qy 340 nGlnLeuGluPheGluArgValTrpGlnLeuPheGlyGluGlyValHisProArgIleGl 360
Db 645 ATGCCAGGAAGATGAATGTGGTTAATGTTGCTGGAACTGGCACTGATCCAAATATTC 704
Qy 360 uGluLeuTyr-GluLysLysLeuAlaProPheLeuSerGlnThrSerHisAsnPheTrps 380
Db 705 AGATGAGTATGGAATACCACTCTGCACCTACCTATCTATAATGAAGATAAATTAATGGC 764
Qy 380 erLysArgLeuTrpTyr 385
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Db 765 CAAGCACTGCTCTTAT 781
RESULT 7
US-09-352-616A-373
; Sequence 373, Application US/09352616A
; Patent No. 6395278
; GENERAL INFORMATION:
; APPLICANT: Dillon, Davin C.
; APPLICANT: Harlocker, Susan Louise
; APPLICANT: Jiang, Yuqi
; APPLICANT: Xu, Jiangchun
; APPLICANT: Mitcham, Jennifer Lynn
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
; FILE REFERENCE: 210121.427C8
; CURRENT APPLICATION NUMBER: US/09/352,616A
; CURRENT FILING DATE: 1999-07-13
; NUMBER OF SEQ ID NOS: 472
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 373
; LENGTH: 1155
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-352-616A-373

Alignment Scores:
Pred. No.: 0.000529 Length: 1155
Score: 118.50 Matches: 66
Percent Similarity: 37.4% Conservative: 19
Best Local Similarity: 29.1% Mismatches: 81
Query Match: 3.4% Indels: 61
DB: 3 Gaps: 11

US-10-620-914-45 (1-648) x US-09-352-616A-373 (1-1155)

```
Qy 187 LeuProLeuArgGlnMetProTrrP-----SerArgArgPhePheTrpArgSerilePhe 204
Db 204 CTTCCCTGCTCCAGGGGAGTGGCAAGACGCTGGCGCTTCTGGAGA----- 254
Qy 205 AspIleAspAenIleAspIleGlyProGluArgAlaTyrLeuGluGlnLysLeuGlu 224
Db 255 -----CCAGCAGCAGCTCTGTAT-----GAA 275
Qy 225 ArgValTrpGluGlnAsnThrGlnGlySerileProTyrValProTrrPLeuArgAlaPro 244
Db 276 GACACTCAGGAACAAGATGGGCAAGTGTGTCCCTGCTGCGAGGGGAG 335
Qy 245 TyrTyrValTrpIleGlyArgLeuProSerValGly---HisAlaLeuHisGluGluArg 263
Db 336 CGGCAAGACCAAGTGGCGCTTGGGAGACTACGATGACAGTGCCTTCATGGAGCCAG 395
Qy 264 ValGluArgProProMetPheProProThrPheLeuTyrThrGlnSerTrp-GluAsp-- 282
Db 396 GTACCACGTCCG-----TGGAGAAGATCT 419
Qy 283 -----ProGluProAspMetGluValMe 290
Db 420 GGACAAGCTCCACAGAGCTGCTGGTGGGTAAAGTCCCAAGAGGATCTCATGTCAT 479
Qy 290 t-----GluIleAsnProLysAsp-----ThrValLeuThrLeuTh 302
Db 480 GCTCAGGACACTGACGTGAACAAGAGGAGGACTGCTCTACATCTGCC 539
Qy 302 rSer-----GlyGlyCysAsnAlaLeuAsnLeuValGlnGlyAlaGlyGlnValVa 320
Db 540 CTCTGCCAATGGGAATTGAGAAGTAGTAAACTCTCTGCTGGACAGCAGATGCAACTTAA 599
Qy 320 lSerValAspCysAsnProAlaGlnSerAlaLeuLeuGluLeuLysLysValAlaIleGl 340
Db 600 TGTCTTGTAC---AACAAAAAGAGGAGCAGCTCTGATAAAG-----GCCGTACA 644
Qy 340 nGlnLeuGluPheGluArgValTrpGlnLeuPheGlyGluGlyValHisProArgIleGl 360
```

```
Db 645 ATCCAGGAGATGAATGTCGTTAATGTTGCTGGAACATGCGCATGATCCAAATATTCC 704
Qy 360 uGluLeuTyr-GluLysLysLeuAlaProPheLeuSerGlnThrSerHisenPheTrpS 380
Db 705 AGATGAGTATGGAATACCACTGCTGCATACGCTATCTATAATGAAGATAAAATTAATGGC 764
Qy 380 erLysArgLeuTyrTyr 385
Db 765 CAAGACACTGCTCTTAT 781

RESULT 8
US-09-289-198-301
; Sequence 301, Application US/09289198
; Patent No. 6586570
; GENERAL INFORMATION:
; APPLICANT: Fridakis, Tony N.
; APPLICANT: Smith, John M.
; APPLICANT: Reed, Steven G.
; APPLICANT: Misher, Lynda
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; TREATMENT OF BREAST CANCER
; FILE REFERENCE: 210121.419C5
; CURRENT APPLICATION NUMBER: US/09/289,198
; CURRENT FILING DATE: 1999-04-09
; EARLIER APPLICATION NUMBER: US 09/062,451
; EARLIER FILING DATE: 1998-04-17
; EARLIER APPLICATION NUMBER: US 08/991,789
; EARLIER FILING DATE: 1997-12-11
; EARLIER APPLICATION NUMBER: US 08/838,762
; EARLIER FILING DATE: 1997-04-09
; EARLIER APPLICATION NUMBER: PCT/US97/00485
; EARLIER FILING DATE: 1997-01-10
; EARLIER APPLICATION NUMBER: US 08/700,014
; EARLIER FILING DATE: 1996-08-20
; EARLIER APPLICATION NUMBER: US 08/585,392
; EARLIER FILING DATE: 1996-01-01
; NUMBER OF SEQ ID NOS: 312
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 301
; LENGTH: 1155
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-289-198-301

Alignment Scores:
Pred. No.: 0.000529 Length: 1155
Score: 118.50 Matches: 66
Percent Similarity: 37.4% Conservative: 19
Best Local Similarity: 29.1% Mismatches: 81
Query Match: 3.4% Indels: 61
DB: 3 Gaps: 11

US-10-620-914-45 (1-648) x US-09-289-198-301 (1-1155)
Qy 187 LeuProLeuArgGlnMetProTyr-----SerArgArgPhePheTyrArgSerIlePhe 204
Db 204 CTTCCCTCTGTCAGCGGGAGTGGCAGACAGACAGTGGCGCTCTCGAGA----- 254
Qy 205 AspIleAspAsnIleAspIleGlyProGluArgArgAlaTyrLeuGluGlnLysLeuGlu 224
Db 255 -----CCACGACGACTCTGCTAT-----GAA 275
Qy 225 ArgValTyrGluGlnAsnThrGlnGlySerIleProTyrValProTyrLeuArgAlaPro 244
Db 276 GACACTCAGGAACAGACAGTGGCAGTGGTGTGCCACTGCTTCCCTGCTGCAGGGGGAG 335
Qy 245 TyrTyrValTyrIleGlyArgLeuProSerValGly---HisAlaLeuHisGluGluArg 263
Db 336 CGGCAAGACAGAGTGGCGCTTGGGGAGACTACATGACAGTGCCTTCATGAGCCCGAG 395
Qy 264 ValGluArgProProMetPheProThrPheLeuTyrThrGlnSerTyr-GluAsp-- 282
Db 396 GTACCACGCTCG-----TGGAGAGAGATCT 419
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Qy 283 -----ProGluProAspMetGluValMe 290
Db 420 GGACAAGCTCCACAGAGCTGCTGGTGGGTAAAGTCCCAAGAGGATCTCATCGTCAT 479
Qy 290 t-----GluIleAsnProLysAsp-----ThrValLeuThrLeuTh 302
Db 480 GCTCAGGAGACATGACGTGACACAGAGGACACAAAGAGGAGTGTCTTACATCTGGC 539
Qy 302 rSer-----GlyGlyCysAsnAlaLeuAsnLeuLeuValGlnGlyAlaGlyGlnValVa 320
Db 540 CTCTGCCAATGGGAATTCAGAAAGTAGTAAAACTCTGCTGCACACAGACGATGTCACACTTAA 599
Qy 320 lSerValAspCysAsnProAlaGlnSerAlaLeuGluLeuLysLysValAlaIleG1 340
Db 600 TGTCTTTGAC---AACAAAAGAGACAGCTCTGATAAAG-----GCCGTACA 644
Qy 340 nGlnLeuGluPheGluAspValTyrGlnLeuPheGlyGlyValHisProArgIleG1 360
Db 645 ATGCCAGGAGATGAATGTGCGTTAATGTTGCTGGAACATGCGCACTGATCCAAATATTCC 704
Qy 360 uGluLeuTyr-GluLysLysLeuAlaProPheLeuSerGlnThrSerHisenPheTrpS 380
Db 705 AGATGAGTATGGAATACCACTGCTGCATACGCTATCTATAATGAAGATAAAATTAATGGC 764
Qy 380 erLysArgLeuTyrTyr 385
Db 765 CAAGACACTGCTCTTAT 781

RESULT 9
US-09-636-215-373
; Sequence 373, Application US/09636215
; Patent No. 6620922
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqui
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TREATMENT OF PROSTATE CANCER
; FILE REFERENCE: 210121.42717C17
; CURRENT APPLICATION NUMBER: US/09/636,215
; CURRENT FILING DATE: 2000-08-10
; NUMBER OF SEQ ID NOS: 852
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 373
; LENGTH: 1155
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-636-215-373

Alignment Scores:
Pred. No.: 0.000529 Length: 1155
Score: 118.50 Matches: 66
Percent Similarity: 37.4% Conservative: 19
Best Local Similarity: 29.1% Mismatches: 81
Query Match: 3.4% Indels: 61
DB: 3 Gaps: 11

US-10-620-914-45 (1-648) x US-09-636-215-373 (1-1155)
```


; GENERAL INFORMATION:
; APPLICANT: Frudakis, Tony N.
; APPLICANT: Smith, John W.
; APPLICANT: Reed, Steven G.
; APPLICANT: Misher, Lynda
; APPLICANT: Retter, Marc W.
; APPLICANT: Dillon, Davin C.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; TREATMENT AND DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 210121.419C6
; CURRENT APPLICATION NUMBER: US/09/429,755A
; CURRENT FILING DATE: 1999-10-28
; NUMBER OF SEQ ID NOS: 315
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 301
; LENGTH: 1155
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-429-755-301

Alignment Scores:
Pred. No.: 0.000529 Length: 1155
Score: 118.50 Matches: 66
Percent Similarity: 37.4% Conservative: 19
Best Local Similarity: 29.1% Mismatches: 81
Query Match: 3.4% Indels: 61
DB: 3 Gaps: 11

US-10-620-914-45 (1-648) x US-09-429-755-301 (1-1155)

Qy 187 LeuProLeuArgGlnMetProTyr-----SerArgArgPhePheTyrArgSerIlePhe 204
Db 204 CTTCCCTGCTGCAGGGGGAGTGGCAAGACAGCAAGCGTGGCGCTCTCGGAGA----- 254
Qy 205 AspileAspAsnIleAspileGlyProGluArgArgAlaTyrLeuGluGlnLysLeuGlu 224
Db 255 -----CCACGACGACTCTCTAT-----GAA 275
Qy 225 ArgValTrpGluGlnAsnThrGlnGlySerIleProTyrValProTyrLeuArgAlaPro 244
Db 276 GACACTCAGGAACAAGATGGGCAAGTGTGTGCCACTGCTTCCCTCTCGAGGGGAG 335
Qy 245 TyrTyrValTrpIleGlyArgLeuProSerValGly---HisAlaLeuHisGluGluArg 263
Db 336 CGGCAAGAGCAAGTGGGGCGCTTGGGAGACATCATGACAGTGCCTTCATGGAGCCGAG 395
Qy 264 ValGluArgProProMetPheProThrPheLeuTyrThrGlnSerTyr-GluAsp-- 282
Db 396 GTACCACGCTCG-----TGAGAGAGATCT 419
Qy 283 -----ProGluProAspMetGluValMe 290
Db 420 GGCAAGCTCCACAGAGCTGCTGGGGTAAAGTCCCAAGAGGATCTCATCGTCAT 479
Qy 290 t-----GluIleAsnProLysAsp-----ThrValLeuThrLeuTh 302
Db 480 GCTCAGGACACTGACTGGAACAGAGAGCAAGCAAGAGGAGTGTCTACATCTGGC 539
Qy 302 rSer-----GlyGlyCysAsnAlaLeuAsnLeuValGlnGlyAlaGlyGlnValVa 320
Db 540 CTCTGCCAATGGGAATTCAGAGTAGTAAATCTCTGTGGACAGACAGCATGTCACACTAA 599
Qy 320 lSerValAspCysAsnProAlaGlnSerAlaLeuLeuGluLysLysValAlaIleG1 340
Db 600 TGTCTCTTGCAC---AACAACAAAGAGGACAGCTCTGATAAG-----GCCGTACA 644
Qy 340 nGlnLeuGluPheGluAspValTrpGlnLeuPheGlyGluGlyValHisProArgIleG1 360
Db 645 ATGCCAGGAAGATGAATGTGGCTTAATGTTCGTGGAACATGGCAGTATCCAAATATTC 704
Qy 360 uGluLeuTyr-GluLysLysLeuAlaProPheLeuSerGlnThrSerHisAsnPheTps 380
Db 705 AGATGAGTATGGAATACCACTCTGCACCTACGCTATCTATATGAAGATAAATTAATGGC 764

Qy 380 erLysArgLeuTyrTyr 385
Db 765 CAAAGCACTGCTCTTAT 781
RESULT 12
US-09-679-426-373
; Sequence 373 Application US/09679426
; Patent No. 6759515
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqui
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedrick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE: 210121.427C20
; CURRENT APPLICATION NUMBER: US/09/679,426
; CURRENT FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 895
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 373
; LENGTH: 1155
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-679-426-373

Alignment Scores:
Pred. No.: 0.000529 Length: 1155
Score: 118.50 Matches: 66
Percent Similarity: 37.4% Conservative: 19
Best Local Similarity: 29.1% Mismatches: 81
Query Match: 3.4% Indels: 61
DB: 3 Gaps: 11

US-10-620-914-45 (1-648) x US-09-679-426-373 (1-1155)

Qy 187 LeuProLeuArgGlnMetProTyr-----SerArgArgPhePheTyrArgSerIlePhe 204
Db 204 CTTCCCTGCTGCAGGGGGAGTGGCAAGACAGCAAGCGTGGCGCTCTCGGAGA----- 254
Qy 205 AspileAspAsnIleAspileGlyProGluArgArgAlaTyrLeuGluGlnLysLeuGlu 224
Db 255 -----CCACGACGACTCTCTAT-----GAA 275
Qy 225 ArgValTrpGluGlnAsnThrGlnGlySerIleProTyrValProTyrLeuArgAlaPro 244
Db 276 GACACTCAGGAACAAGATGGGCAAGTGTGTGCCACTGCTTCCCTCTCGAGGGGAG 335
Qy 245 TyrTyrValTrpIleGlyArgLeuProSerValGly---HisAlaLeuHisGluGluArg 263
Db 336 CGGCAAGAGCAAGTGGGGCGCTTGGGAGACTACGATGACAGTGCCTTCATGGAGCCGAG 395
Qy 264 ValGluArgProProMetPheProThrPheLeuTyrThrGlnSerTyr-GluAsp-- 282
Db 396 GTACCACGCTCG-----TGAGAGAGATCT 419
Qy 283 -----ProGluProAspMetGluValMe 290
Db 420 GGCAAGCTCCACAGAGCTGCTGGGGTAAAGTCCCAAGAGGATCTCATCGTCAT 479


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QY 290 t-----GlulleAsnProLysAsp-----ThrValLeuThrLeuTh 302
Db | : : : : : | | | | | | | | | | | | | | | | | | | | | |
480 GCTCAGGACACTGACGTGAACAAGAGGACAAAGAGGAGGACTGCTCTACATCTGC 539
QY 302 rSer-----GlyGlyCysAsnAlaLeuAsnLeuValGlnGlyAlaGlyGlnValVa 320
Db | : : : : : | | | | | | | | | | | | | | | | | | | | | |
540 CTCTGCCAATGGGAATTTCAGAAAGTAGTAAACTCTCTGGACACAGCATGTCAACTTAA 599
QY 320 lSerValAspCysAsnProAlaGlnSerAlaLeuLeuGluLeuLysValAlaIleG1 340
Db | : : : : : | | | | | | | | | | | | | | | | | | | | | |
600 TGTCTCTGAC---AACAAAAGAGGACAGCTCTGATAAAG-----GCCGTACA 644
QY 340 nGlnLeuGluPheGluAspValTrpGlnLeuPheGlyGluGlyValHisProArgIleG1 360
Db | : : : : : | | | | | | | | | | | | | | | | | | | | | |
645 ATGCCAGGAAGATGAATGTCGTTAATGTTGCTGGAACATGCGCATGATCCAAATATTC 704
QY 360 uGluLeuTyr-GluLysLysLeuAlaProPheLeuSerGlnThrSerHisPheTrpS 380
Db | : : : : : | | | | | | | | | | | | | | | | | | | | | |
705 AGATGAGTATGGAATACCACTCTGCACTACGCTATCTATTAATGAAGATAAATTAATGC 764
QY 380 erLysArgLeuTrpTyr 385
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | |
765 CAAGCACTGCTCTTAT 781
```

RESULT 13

US-09-759-143-373
; Sequence 373, Application US/09759143
; Patent No. 6800746

; GENERAL INFORMATION:

; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqui
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedwick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.

; APPLICANT: Hepler, William
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER

; FILE REFERENCE: 210121.427C23

; CURRENT APPLICATION NUMBER: US/09/759,143

; CURRENT FILING DATE: 2001-01-12

; NUMBER OF SEQ ID NOS: 934

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 373

; LENGTH: 1155

; TYPE: DNA

; ORGANISM: Homo sapien

US-09-759-143-373

Alignment Scores:

Pred. No.:	0.000529	Length:	1155
Score:	118.50	Matches:	66
Percent Similarity:	37.4%	Conservative:	19
Best Local Similarity:	29.1%	Mismatches:	81
Query Match:	3.4%	Indels:	61
Db:	3	Gaps:	11

US-10-620-914-45 (1-648) x US-09-759-143-373 (1-1155)

QY 187 LeuProLeuArgGlnMetProTrp-----SerArgPhePheTrpArgSerIlePhe 204

Db 204 CTTCCCTGCTGCAGGGGAGTGGCAAGCAACGTCGGCGCTTCTGGAGA----- 254

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QY 205 AspileAspAsnIleAspileGlyProGluArgArgAlaTyrLeuGluGlnLysLeuGlu 224
Db | : : : : : | | | | | | | | | | | | | | | | | | | | | |
255 -----CCACGACGACTCTGCTAT-----GAA 275
QY 225 ArgValTrpGluGlnAsnThrGlnGlySerIleProTyrValProTrpLeuArgAlaPro 244
Db | : : : : : | | | | | | | | | | | | | | | | | | | | | |
276 GACACTCAGGAACAAGATGGGCAAGTGTGTGCCACTGCTTCCCTCTGTCGAGGGGGAG 335
QY 245 TyrTrpValTrpIleGlyArgLeuProSerValGly---HisAlaLeuHisGluGluArg 263
Db | : : : : : | | | | | | | | | | | | | | | | | | | | | |
336 CGCAAGACCAAGTGGGGGCTTGGGGAGACTACCATGACAGTGCCTTCATCGAGCCAG 395
QY 264 ValGluArgProProMetPheProProTrpPheLeuTyrThrGlnSerTrp-GluAsp-- 282
Db | : : : : : | | | | | | | | | | | | | | | | | | | | | |
396 GTACCACGTCGG-----TGGAAGAAGATCT 419
QY 283 -----ProGluProAspMetGluValMe 290
Db | : : : : : | | | | | | | | | | | | | | | | | | | | | |
420 GGACAAGCTCCACAGAGCTGCTGGTGGGTAAGATCCCAAGAGGATCTCATCGTCAT 479
QY 290 t-----GlulleAsnProLysAsp-----ThrValLeuThrLeuTh 302
Db | : : : : : | | | | | | | | | | | | | | | | | | | | | |
480 GCTCAGGACACTGACGTGAACAAGAGGACAAAGAGGAGGACTGCTCTACATCTGC 539
QY 302 rSer-----GlyGlyCysAsnAlaLeuAsnLeuValGlnGlyAlaGlyGlnValVa 320
Db | : : : : : | | | | | | | | | | | | | | | | | | | | | |
540 CTCTGCCAATGGGAATTTCAGAAAGTAGTAAACTCTCTGGACACAGCATGTCAACTTAA 599
QY 320 lSerValAspCysAsnProAlaGlnSerAlaLeuLeuGluLeuLysValAlaIleG1 340
Db | : : : : : | | | | | | | | | | | | | | | | | | | | | |
600 TGTCTCTGAC---AACAAAAGAGGACAGCTCTGATAAAG-----GCCGTACA 644
QY 340 nGlnLeuGluPheGluAspValTrpGlnLeuPheGlyGluGlyValHisProArgIleG1 360
Db | : : : : : | | | | | | | | | | | | | | | | | | | | | |
645 ATGCCAGGAAGATGAATGTCGTTAATGTTGCTGGAACATGCGCATGATCCAAATATTC 704
QY 360 uGluLeuTyr-GluLysLysLeuAlaProPheLeuSerGlnThrSerHisPheTrpS 380
Db | : : : : : | | | | | | | | | | | | | | | | | | | | | |
705 AGATGAGTATGGAATACCACTCTGCACTACGCTATCTATTAATGAAGATAAATTAATGC 764
QY 380 erLysArgLeuTrpTyr 385
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | |
765 CAAGCACTGCTCTTAT 781
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RESULT 14

US-09-651-236-373
; Sequence 373, Application US/09651236
; Patent No. 6818751

; GENERAL INFORMATION:

; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqui
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedwick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.

; APPLICANT: Hepler, William

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER

; FILE REFERENCE: 210121.42718C18

; CURRENT APPLICATION NUMBER: US/09/651,236

; CURRENT FILING DATE: 2000-08-29

; NUMBER OF SEQ ID NOS: 865

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; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 373
; LENGTH: 1155
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-651-236-373

Alignment Scores:
Pred. No.: 0.000529 Length: 1155
Score: 118.50 Matches: 66
Percent Similarity: 37.4% Conservative: 19
Best Local Similarity: 29.1% Mismatches: 81
Query Match: 3.4% Indels: 61
DB: 3 Gaps: 11

US-10-620-914-45 (1-648) x US-09-651-236-373 (1-1155)

Qy 187 LeuProLeuArgGlnMetProTrrp-----SerArgArgPhePheTrpArgSerilePhe 204
Db 204 CTTCCCTGCTGCAGGGGAGTGGCAAGACGCTGGGGCGCTTCTGGAGA-----254
Qy 205 AspileAspAenileAspileGlyProGluArgAlaTyrLeuGluGlnLysLeuGlu 224
Db 255 -----CCACGACGACTCTGCTAT-----GAA 275
Qy 225 ArgValTrrpGluGlnAenThrGlnGlySerileProTrrpValProTrrpLeuArgAlaPro 244
Db 276 GACACTCAGGAACAGAGTGGCAAGTGTGTCTGCCACTGCTTCCCTGCTGCGGGGAG 335
Qy 245 TyrTrrpValTrrpIleGlyArgLeuProSerValGly---HisAlaLeuHisGluGluArg 263
Db 336 CGGCAAGACGAGTGGGGCGCTTGGGAGACTACGATGACAGTGCCTTCATGGAGCCAG 395
Qy 264 ValGluArgProProMetPheProProThrPheLeuTyrThrGlnSerTrp-GluAsp-- 282
Db 396 GTACCACGCTCGG-----TGAGAGAAGATCT 419
Qy 283 -----ProGluProAspMetGluValMe 290
Db 420 GGACAAAGTCCACAGAGTGGCTGGTGGGTAAAGTCCCGAAGAGATCTCATGTCAT 479
Qy 290 t-----GluIleAsnProLysAsp-----ThrValLeuThrLeuTh 302
Db 480 GCTCAGGACACTGACGCTGAGCAAGAGGACAAAGCAAGAGGAGGACTGCTTACATCTGC 539
Qy 302 rSer-----GlyGlyCysAsnAlaLeuAsnLeuValGlnGlyAlaGlyGlnValVa 320
Db 540 CTCTGCCAATGGGAATTCAGAAAGTAGTAAACTCTCTGTCGACAGACGATGTCAACTTAA 599
Qy 320 lSerValAspCysAsnProAlaGlnSerAlaLeuLeuGluLysLysValAlaIleGl 340
Db 600 TGTCTTTGAC---AACAAAAGAGGAGGACGCTGTATAAG-----GCCGTACA 644
Qy 340 nGlnLeuGluPheGluAspValTrrpGlnLeuPheGlyGluGlyValHisProArgIleGl 360
Db 645 ATGCCAGGAGATGAATGTGGGTTAATGTGTGGAAACATGCGACTGTATCCAAATATCC 704
Qy 360 uGluLeuTyr-GluLysLysLeuAlaProPheLeuSerGlnThrSerHisAsnPheTrps 380
Db 705 AGATGAGTATGGAAATACCACTCTGCACTCTGCTATCTATATAATGAAGATAAATTAATG 764
Qy 380 erLysArgLeuTrrpTyr 385
Db 765 CAAGCACTGCTCTTAT 781
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RESULT 15

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US-09-699-295-301
; Sequence 301, Application US/09699295
; Patent No. 6828431
; GENERAL INFORMATION:
; APPLICANT: Fridakis, Tony N.
; APPLICANT: Reed, Steven G.
; APPLICANT: Smith, John M.
```

```
; APPLICANT: Misher, Linda E.
; APPLICANT: Dillon, Davin C.
; APPLICANT: Retter, Marc W.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Harlocker, Susan L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; TREATMENT OF BREAST CANCER
; FILE REFERENCE: 210121.419C10
; CURRENT APPLICATION NUMBER: US/09/699,295
; CURRENT FILING DATE: 2000-10-26
; NUMBER OF SEQ ID NOS: 326
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 301
; LENGTH: 1155
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-699-295-301

Alignment Scores:
Pred. No.: 0.000529 Length: 1155
Score: 118.50 Matches: 66
Percent Similarity: 37.4% Conservative: 19
Best Local Similarity: 29.1% Mismatches: 81
Query Match: 3.4% Indels: 61
DB: 3 Gaps: 11

US-10-620-914-45 (1-648) x US-09-699-295-301 (1-1155)

Qy 187 LeuProLeuArgGlnMetProTrrp-----SerArgArgPhePheTrpArgSerilePhe 204
Db 204 CTTCCCTGCTGCAGGGGAGTGGCAAGACGCTGGGGCGCTTCTGGAGA-----254
Qy 205 AspileAspAenileAspileGlyProGluArgAlaTyrLeuGluGlnLysLeuGlu 224
Db 255 -----CCACGACGACTCTGCTAT-----GAA 275
Qy 225 ArgValTrrpGluGlnAenThrGlnGlySerileProTrrpValProTrrpLeuArgAlaPro 244
Db 276 GACACTCAGGAACAGAGTGGCAAGTGTGTCTGCCACTGCTTCCCTGCTGCGGGGAG 335
Qy 245 TyrTrrpValTrrpIleGlyArgLeuProSerValGly---HisAlaLeuHisGluGluArg 263
Db 336 CGGCAAGACGAGTGGGGCGCTTGGGAGACTACGATGACAGTGCCTTCATGGAGCCAG 395
Qy 264 ValGluArgProProMetPheProProThrPheLeuTyrThrGlnSerTrp-GluAsp-- 282
Db 396 GTACCACGCTCGG-----TGAGAGAAGATCT 419
Qy 283 -----ProGluProAspMetGluValMe 290
Db 420 GGACAAAGTCCACAGAGTGGCTGGTGGGTAAAGTCCCGAAGAGATCTCATGTCAT 479
Qy 290 t-----GluIleAsnProLysAsp-----ThrValLeuThrLeuTh 302
Db 480 GCTCAGGACACTGACGCTGAGCAAGAGGACAAAGCAAGAGGAGGACTGCTTACATCTGC 539
Qy 302 rSer-----GlyGlyCysAsnAlaLeuAsnLeuValGlnGlyAlaGlyGlnValVa 320
Db 540 CTCTGCCAATGGGAATTCAGAAAGTAGTAAACTCTCTGTCGACAGACGATGTCAACTTAA 599
Qy 320 lSerValAspCysAsnProAlaGlnSerAlaLeuLeuGluLysLysValAlaIleGl 340
Db 600 TGTCTTTGAC---AACAAAAGAGGAGGACGCTGTATAAG-----GCCGTACA 644
Qy 340 nGlnLeuGluPheGluAspValTrrpGlnLeuPheGlyGluGlyValHisProArgIleGl 360
Db 645 ATGCCAGGAGATGAATGTGGGTTAATGTGTGGAAACATGCGACTGTATCCAAATATCC 704
Qy 360 uGluLeuTyr-GluLysLysLeuAlaProPheLeuSerGlnThrSerHisAsnPheTrps 380
Db 705 AGATGAGTATGGAAATACCACTCTGCACTCTGCTATCTATATAATGAAGATAAATTAATG 764
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Qy 380 erLysargLeuTrpTyr 385
|||
Db 765 CAAGCACTGCTCTTAT 781

Search completed: May 4, 2006, 17:45:16
Job time : 334 secs

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GenCore version 5.1.7
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OM protein - nucleic search, using frame_plus_p2n model

Run on: May 4, 2006, 17:40:29 ; Search time 1360 Seconds
(without alignments)
3940.115 Million cell updates/sec

Title: US-10-620-914-45

Perfect score: 3463

Sequence: 1 MGSRGDRPASVTKNFSL.....RVNYSFYMARRKAKKDN 648

Scoring table:

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Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Published Applications NA Main:

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2: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq.*
3: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq.*
4: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq.*
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8: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq.*
9: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq.*
10: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3463	100.0	1947	7	US-10-620-914-44
2	2838	82.0	5242	7	US-10-620-914-43
3	891	25.7	2259	8	US-10-741-849-6021
4	850.5	24.6	2727	7	US-10-620-914-49
5	804	23.2	3427	7	US-10-620-914-48
6	379.5	11.0	1252	5	US-10-118-495-1
7	379.5	11.0	1252	5	US-10-620-914-1

8	329	9.5	1248	5	US-10-118-495-22	Sequence 22, Appl
9	329	9.5	1248	7	US-10-620-914-22	Sequence 22, Appl
10	326.5	9.4	1251	5	US-10-118-495-28	Sequence 28, Appl
11	326.5	9.4	1251	7	US-10-620-914-28	Sequence 28, Appl
12	292.5	8.4	1251	5	US-10-118-495-32	Sequence 32, Appl
13	292.5	8.4	1251	7	US-10-620-914-32	Sequence 32, Appl
14	128	3.7	4246	6	US-10-085-959-12	Sequence 52, Appl
15	123	3.6	7119	8	US-10-684-141-57	Sequence 57, Appl
16	123	3.6	7119	9	US-10-810-486-57	Sequence 34, Appl
17	120	3.5	666	5	US-10-118-495-34	Sequence 34, Appl
18	120	3.5	666	7	US-10-620-914-34	Sequence 34, Appl
19	119	3.4	6912	8	US-10-335-053-309	Sequence 309, Appl
20	119	3.4	6912	8	US-10-684-141-53	Sequence 53, Appl
21	119	3.4	6912	9	US-10-810-486-53	Sequence 53, Appl
22	119	3.4	6912	9	US-10-887-553A-400	Sequence 400, Appl
23	118.5	3.4	1155	3	US-09-825-301-5	Sequence 5, Appl
24	118.5	3.4	1155	3	US-09-759-143-373	Sequence 373, Appl
25	118.5	3.4	1155	3	US-09-780-669-373	Sequence 373, Appl
26	118.5	3.4	1155	3	US-09-810-936-301	Sequence 301, Appl
27	118.5	3.4	1155	3	US-09-822-827-373	Sequence 373, Appl
28	118.5	3.4	1155	3	US-09-429-755-301	Sequence 301, Appl
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30	118.5	3.4	1155	3	US-09-895-793-373	Sequence 373, Appl
31	118.5	3.4	1155	3	US-09-895-814-373	Sequence 373, Appl
32	118.5	3.4	1155	5	US-10-012-896-373	Sequence 373, Appl
33	118.5	3.4	1155	5	US-10-010-940-373	Sequence 373, Appl
34	118.5	3.4	1155	6	US-10-212-679-301	Sequence 301, Appl
35	118.5	3.4	1155	6	US-10-144-678A-373	Sequence 373, Appl
36	118.5	3.4	1155	6	US-10-033-527-5	Sequence 5, Appl
37	118.5	3.4	1155	6	US-10-294-025-373	Sequence 373, Appl
38	118.5	3.4	1155	7	US-10-079-137B-301	Sequence 301, Appl
39	118.5	3.4	1185	3	US-09-924-400-335	Sequence 335, Appl
40	118.5	3.4	1185	6	US-10-212-679-335	Sequence 335, Appl
41	118.5	3.4	1185	7	US-10-079-137B-335	Sequence 335, Appl
42	118.5	3.4	1383	3	US-09-905-673-64	Sequence 64, Appl
43	118.5	3.4	1383	6	US-10-096-319-65	Sequence 64, Appl
44	118.5	3.4	1434	3	US-09-905-673-65	Sequence 65, Appl
45	118.5	3.4	1434	6	US-10-096-319-65	Sequence 65, Appl

ALIGNMENTS

RESULT 1

US-10-620-914-44
; Sequence 44, Application US/10620914
; Publication No. US20040093639A1
; GENERAL INFORMATION:
; APPLICANT: Benning, Christoph
; APPLICANT: Riekhof, Wayne
; APPLICANT: Klug, Rouven
; TITLE OF INVENTION: Compositions and Methods for the Production of Betaine Lipids
; FILE REFERENCE: MSU-07769
; CURRENT APPLICATION NUMBER: US/10/620,914
; CURRENT FILING DATE: 2003-07-16
; PRIOR FILING DATE: 2002-04-08
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 44
; TYPE: DNA
; ORGANISM: Chlamydomonas reinhardtii
US-10-620-914-44

Alignment Scores:				
Pred. No.:	0	Length:	1947	
Score:	3463.00	Matches:	648	
Percent Similarity:	100.0%	Conservative:	0	
Best Local Similarity:	100.0%	Mismatches:	0	
Query Match:	100.0%	Indels:	0	
DB:	7	Gaps:	0	
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Qy 21 LysLeuLysLeuSerSerMetLysAspAspLeuThrValLeuArgHisMetTrpPheGly 40
Db 61 AAGCTCAAGCTCAGCAGCATGAGGATGACCTGACCGTTCCTGCGCCATATGTGGTTCCGC 120
Qy 41 SerLysLysGlyAspAspHisAlaAlaArgLeuGluSerPheTyrGlyProGlnAlaAla 60
Db 121 AGCAAGAAGGGCGATGATCACTGCTGCTCGAGAGCTTCTACGGGCGCCAGGCGCT 180
Qy 61 AlaPheAlaAlaArgLeuAlaGluArgSerAsnLeuIleTrpValAspLeuGlyGly 80
Db 181 GCCTTTGCTGCCCGCTGGCGAGCGCTCGAACCTCATCTGGGTTGACCTGGGTTGGTGGC 240
Qy 81 ThrGlyGluAsnValAspMetMetAlaAspTyrIleAspLeuAlaLysPheLysSerIle 100
Db 241 ACTGGGAGAGATGTCGATATGATGGCTGATTACATCGACCTGGCGAAGTTCAGTCCATC 300
Qy 101 TyrValValAspLeuLysHisSerLeuCysGluValAlaLysLysLysAlaLysAlaLys 120
Db 301 TACGTGGTCGACCTGTGCCTGCTGCGAGGTGGCCAAAGAAAGAGCGCAAGGCCAAG 360
Qy 121 GlyTrpLysAsnValGlnValAlaAlaAspAlaCysGlnPheAlaProGluGly 140
Db 361 GGCTGGAGAGATGCCAGGTGCTGAGGCCGACGCTTGCCAAATTTGCGCCCCCTTGAGGGC 420
Qy 141 ThrAlaThrLeuIleThrPheSerTyrSerLeuThrMetIleProProPheHisAsnVal 160
Db 421 ACCGGAGGCTCATCACCTTCTCCTACTCGTACAGATGATTCACCGTTCCACACAGTC 480
Qy 161 IleAspGlnAlaCysSerTyrLeuSerGlnAspGlyLeuValGlyValAlaAspPheTyr 180
Db 481 ATCGACACAGGCTGCTCGTCTGTCCCAAGACGGCTGGTGGGCGTTCGCGACTTCTAC 540
Qy 181 ValSerGlyLysTyrAspLeuProLeuArgGlnMetProTrpSerArgPhePheTrp 200
Db 541 GTGAGCGGCAGTACGACCTGCCCTCGCGCAGATGCCCTTGGTCGCGCGTTCTTCGG 600
Qy 201 ArgSerIlePheAspIleAspAsnIleAspIleGlyProGluArgArgAlaTyrLeuGlu 220
Db 601 CGATCGATCTTCGACATCGACCAATTCATTCGCCCCGAGCGCGCGCTACTCTGGAG 660
Qy 221 GlnLysLeuGluArgValTrpGluGlnAsnThrGlnGlySerIleProTyrValProTrp 240
Db 661 CAGAAGCTGGAGCGCGCTGTGGGAGCAGAACACCCAGGGTTGATCCCCCTACGTGCGGTG 720
Qy 241 LeuArgAlaProTyrTyrValTrpIleGlyArgLeuProSerValGlyHisAlaLeuHis 260
Db 721 CTGGCGCCCCCTACTACTGTGGATTGGCCCTGCCCCCTGCGAGGTGGCCAGCCCCGTGAC 780
Qy 261 GluGluArgValGluArgProMetPheProProThrPheLeuTyrThrGlnSerTrp 280
Db 781 GAGGAGCGCGTGGAGCGCGCCGCAATGTTCCGCCCCACCTTCTCTGTACACGACGTCTGG 840
Qy 281 GluAspProGluProAspMetGluValMetGluIleAsnProLysAspThrValLeuThr 300
Db 841 GAGGACCCCGAGCGCGATATGGAGGTGATGGAGATCAACCCCAAGGACACGCGTGTGACC 900
Qy 301 LeuThrSerGlyGlyCysAsnAlaLeuAsnLeuValGlnGlyValAlaGlyGlnValVal 320
Db 901 CTGACTACGGCGGCTGCAATGCCCTGAACTGCTGGTGGAGGGGGCGCGCAGGTGGTG 960
Qy 321 SerValAspCysAsnProAlaGlnSerAlaLeuLeuGluLeuLysLysValAlaIleGln 340
Db 961 TCGGTGGACTCAACCCCGCAGTCCGCGCTTCTGGAGCTGAAGAAGGTGGCCATTCCAG 1020
Qy 341 GlnLeuGluPheGluAspValTrpGlnLeuPheGlyGluGlyValHisProArgIleGlu 360
Db 1021 CAGCTGGAGTTTGGAGCAGTGTGGCAGCTGTTGCGCGAGGGCGTGCACCCGCGATTGAG 1080

Qy 361 GluLeuTyrGluLysLysLeuAlaProPheLeuSerGlnThrSerHisAsnPheTrpSer 380
Db 1081 GAGCTGTACGAGAAAGAGCTGGCGCCCTTCTCTGTGCAAAACGACCAACAATCTTGTGTCC 1140
Qy 381 LysArgLeuTrpTyrPheGlnHisGlyLeuTyrTyrGlnGlyGlyMetGlyLysLeuCys 400
Db 1141 AAGCGCTCTGTTACTTCCAGCAGCGCTGTACTACCAAGGCGCGCATGGCGAAGCTGTGC 1200
Qy 401 TrpValLeuGlnCysLeuAlaValValLeuGlyLeuGlyLysThrValLysArgLeuAla 420
Db 1201 TGGGTGCTGAGTGCCTGGCGCTGGTGTGGGACTGGGCAAGCGTCAAGCGGCTCGCC 1260
Qy 421 AsnAlaProThrMetGluGluGlnArgArgLeuTrpAspSerAsnMetLeuIleHisPhe 440
Db 1261 AACCGCCCAACATGAGGAGCAGCGCGTCTGTGGGACAGCAATGCTCATCCACTTC 1320
Qy 441 ValLysAsnGlyProLysProLeuValTrpLeuPheValLysPheValSerLeuValLeu 460
Db 1321 GTGAAGAACGGGCCCCAAGCGCTGTTGTGGTGTTCGTCAAGTTCTGTGAGCTGTGTGCTC 1380
Qy 461 PheAsnLysAlaValLeuTrpPheGlyGlyValProGlyLysGlnTyrAlaLeuIle 480
Db 1381 TTCAACAGGCGCTGCTGTGGTTCGGCGCGCGCGTGGCGGCAAGCAGTACGCGCTGATC 1440
Qy 481 LysAlaAspGlyIleProIleGluAsnTyrIleAlaArgThrMetAspGlyValAlaGlu 500
Db 1441 AAGCGGAGCGCATCCCATTTGAGACTACATCGCGCGCACCATGGACGGCGTGGCGAG 1500
Qy 501 AsnSerHisValArgLysGlnAsnTyrPheTyrTyrAsnCysLeuThrGlyLysPheLeu 520
Db 1501 AACTCGCACGTCGCAAGCAGAACTACTTCTTACTACAACTGCCTCACCGGCAAGTTCCTG 1560
Qy 521 ArgAspAsnCysProThrTyrLeuArgGluAlaAlaPheAlaThrLeuLysSerGlyVal 540
Db 1561 CGCGACAACTGCCCCACCTACTCGCGAGCGCGCTTCGCCACCTCAAGAGTGGCGTG 1620
Qy 541 ValAspAsnLeuThrValSerThrAsnPhePheMetGluGluLeuLysAlaArgThrTyr 560
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Qy 561 ThrLysValIleLeuMetAspHisValAspTrpLeuAspMetProValAlaAsnGluLeu 580
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Db 1741 GCCAGTGCCTGGCCCAAGCAGGTTCGCGCGGCGGCAFCATCTGCGCTTCGCCCTCC 1800
Qy 601 LeuSerProProTyrAlaGluLeuIleGlnLysAlaGlyPheAspValArgCysIleArg 620
Db 1801 CTCAGCGCGCTACGCGAGCTGATCCAGAAGGGGGCTTCGACGTGCGCTGCATCCGC 1860
Qy 621 ArgAlaThrGlnGlyTyrMetAspArgValAsnMetTyrSerSerPheTyrMetAlaArg 640
Db 1861 CGCGCCACTCAGGGCTACATGGACCGCGTCAACATGTATACAGCTCCTTCTATATGCCCGC 1920
Qy 641 ArgLysGlyAlaLysLysAspAsn 648
Db 1921 CGGAAGGGCGCCCAAGAGGACAAC 1944

RESULT 2

US-10-620-914-43

; Sequence 43, Application US/10620914

; Publication No. US20040093639A1

; GENERAL INFORMATION:

; APPLICANT: Benning, Christoph

; APPLICANT: Riekhof, Wayne

; APPLICANT: Klug, Rouven

; TITLE OF INVENTION: Compositions and Methods for the Production of Betaine Lipids

; FILE REFERENCE: MSU-07769

; CURRENT APPLICATION NUMBER: US/10/620,914

; CURRENT FILING DATE: 2003-07-16

; PRIOR APPLICATION NUMBER: 10/118,495

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; PRIOR FILING DATE: 2002-04-08
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 43
; LENGTH: 5242
; TYPE: DNA
; ORGANISM: Chlamydomonas reinhardtii
US-10-620-914-43

Alignment Scores:
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Score: 2838.00 Matches: 645
Percent Similarity: 45.6% Conservative: 0
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Query Match: 82.0% Indels: 771
DB: 7 Gaps: 11

US-10-620-914-45 (1-648) x US-10-620-914-43 (1-5242)

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Qy 21 LysLeuLysLeuSerSerMetLysAspAspLeuThrValLeuArgHisMetTrpPheGly 40
Db 561 AAGCTCAAGCTCAGCAGCATGAAGATGACCTGACCGTCTCGCGCCATATGTGTTCGGC 620

Qy 41 SerLysLysGlyAspAspHisAlaAlaArgLeuGluSerPheTyrGlyProGlnAlaAla 60
Db 621 AGCAAGAAGGGGATGATCAGCTGCTGCTCGCTGGAGACTTCTACGGGCCCCAGCGCGCT 680

Qy 61 AlaPhe----- 62
Db 681 GCCTG-TAAGTCGGGATTAACTTTATGTCTCATTTAAGTTGTTTCGAGTTGCTTACGCGCTG 739

Qy 62 ----- 62
Db 740 TCTGCGCGCGCAGATGATGCTTTTCGGTTCGGGTTCCTCTCGGGTTCGAGGCCCATGCTC 799

Qy 63 -----AlaAlaArgLeuAlaGluArgSerAsnLeuLeuTrpValAspLeuGlyGly 79
Db 800 GCTGCAAGTTGCTGCCCGCTGCGCGAGCGCTCGAACCTCATCTGGTTGACTTGGTGGT 859

Qy 80 GlyThrGly----- 82
Db 860 GGCACCTGGGTGAGTCGCGGTGTGATCGGGAGGTGCGGGATAGCCCTCGCGCTTGGCT 919

Qy 83 -----GluAsnVal 85
Db 920 GCGCTCGCGCGCATTTATGCTGATCTGCGCTTTGCTTTTGTGCGCGCAGAGAAATGTC 979

Qy 86 AspMetMetAlaAspTyrIleAspLeuAlaLysPheLysSerIleTyrValValAspLeu 105
Db 980 GATATGATGGCTGATTATCATCGACTGGCGAAGTTCAAGTCCATCATCTAGTGGTGCACCTG 1039

Qy 106 CysHisSerLeuCysGluValAlaLysLysLysAlaLysAlaLysGlyTyrLysAsnVal 125
Db 1040 TGCCACTCGCTGTGCGAGGTGCCCAAGAAGAAGCGAAGGCCAAGGGCTGGAAGAATGTC 1099

Qy 126 GlnValValGluAlaAspAlaCysGlnPheAlaProProGluGlyThrAlaThrLeuIle 145
Db 1100 CAGTCTGTGGAGGCGCGCTTGGCAATTTTCGCCCTTCGAGGCGACCGCGACGCTCATC 1159

Qy 146 ThrPheSerTyrSerLeuThrMet----- 153
Db 1160 ACCTTCTCTACTCGTCAACAG-TGAGTTGCAAGCGCGTTCGACTTGCCATCGGAGGATC 1218

Qy 154 -----IlePro 155
Db 1219 CATCCACCCACAACGTTTCATCCCTCTCACCCCGCGCTTTTGTGTTGCAATGATTTCCA 1278

Qy 156 ProPheHisAsnValIleAspGlnAlaCysSerTyrLeuSerGlnAspGlyLeuValGly 175
Db 1561 ATGGGGTTCGGTTCGTGACGGCGCGCTCGAGCTACACCAAGAAGAACTTCTCCCTGGAG 560
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Db 1279 CCGTTCACAACAGTCATCGACCGCTTGTCTGTACCTGTCCCAAGACGGCCTGGTGGGC 1338
Qy 176 ValAlaAspPheTyrValSerGlyLysTyrAspLeuProLeuArgGlnMetProTrpSer 195
Db 1339 GTTGCCGACTTCTACGTGAGCGGCAAGTAGACCTGCCCCCTGCGCCAGATGCCCTGGTTCG 1398
Qy 196 ArgArgPhePheTrp----- 200
Db 1399 CGCGGTTTCTTCTGCGGTGAGTTACCAGGCCGCGGTACACATCTCTCAAGCAAGCGTA 1458
Qy 200 ----- 200
Db 1459 GCTGAGCGGGGCACAGAAGCGCTTAGGGCCCGGGTCCGCTTCTGGGTAGTGGCAAGGA 1518
Qy 200 ----- 200
Db 1519 TATCGCAAGGCCCTTTCAGCTACCCGAGTACCAGGTATGATGTGTGTACGACGACTCATCAC 1578
Qy 200 ----- 200
Db 1579 GGTGCTGACTGAGGACACGTGCTCGAGTCTGCGGTCTCATAGGGCTTTTCAGCACATACA 1638
Qy 200 ----- 200
Db 1639 GCGCAGTCTCCGAATGCGGTGTGTGACGCTGTATGTCTCCGGGACAGCACCATGCACCGT 1698
Qy 200 ----- 200
Db 1699 GCGCGGTTCTTGACTTGCATCCGCTGCTCTCGGGCTCCCTGGGTTCGCTCAGACACGT 1758
Qy 201 -----ArgSerIlePheAspIleAsn 208
Db 1759 CTCGCTGCCCCGTGTGTCTGCTGCTGTGTGTGTCAGATCGATCTTCGACATCGACAAAC 1818
Qy 209 IleAspIleGlyProGluArgAlaTyrLeuGluGlnLysLeuGluValTrpGlu 228
Db 1819 ATTGACATCGCCCCGAGCGCGCTTACTGTGAGCAGAAGCTGGAGCGCGGTGGGAG 1878
Qy 229 GlnAsnThr----- 231
Db 1879 CAGAACACCCAGGTTGTGCGCGTTGTGACACTGCTGCTGTGCAAGCCCAAGTAAGTTTG 1938
Qy 231 ----- 231
Db 1939 CTCATCAGCCCTGCGACACCGCGCGGTGCGGGGATATTCATCGGACAGACCGTCCGCA 1998
Qy 232 -----GlnGlySerIlePro 236
Db 1999 CTGTTGGTTAATCCACACGATCCGCTGCCCTTCTCTGCGGTTCAGGGTTCCATCCCC 2058
Qy 237 TyrValProTrpLeuArgAlaProTyrTyrValTrpIleGlyArgLeuProSerValGly 256
Db 2059 TAGGTGCGGTGGCTGCGCGCCCCCTACTAGTGTGGATTGCGCGCTGCCCGAGCGTTGGC 2118
Qy 257 His----- 257
Db 2119 CG-TGAGTTCGCGTTCGCGCGGACCTCGTCCGATCAGGACACATGGTTACGGGGCCCTCA 2177
Qy 257 ----- 257
Db 2178 GTGAAGCGTATCGTATCGTTGACAGTCTGTCACAGCGTACCACAAAGCGCGTCCCTTG 2237
Qy 257 ----- 257
Db 2238 CGCGTTGAATTTGTCGCGCAAGCATGACCGTGGCGCGATGCCCAACTCGCGTTGAC 2297
Qy 258 -----AlaLeuHisGluGluArgValGluArgProProMetPheProProThrPhe 274
Db 2298 CCTGCAGACGCGCTGCACGAGGCGGTGGAGCGCGCGCCCATGTTCCCGCCACCTTC 2357
Qy 275 LeuTyrThrGlnSerTrpGluAspProGluProAspMetGlu----- 288
Db 2358 CTGTACACGCGATCGTGGGAGGACCCCGAGCCGATATGGAGGTGAGCGGCTCAGCCTGA 2417
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Db 4578 TGTTCGGATAACGGAAGCGAACCTAGCGTCAGGGCGCAACAGCGCGTGGCGCACCGCCGAAA 4637
 Qy 634 -----Ser 634
 Db 4638 TCTCGTTGTCTTCGATGTATACCTGATCCCACTTTGTCGGTTTCTCCCAATGGCAGC 4697
 Qy 635 SerPheTyrMetAlaArgAlaGlyGlyAlaLysLysAspAsn 648
 Db 4698 TCCTTACATGGCCCGCGAAGGGCGCCCAAGAAGGACAAC 4739
 RESULT 3
 US-10-741-849-6021
 ; Sequence 6021, Application US/10741849
 ; Publication No. US20050019931A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Roemer, Terry
 ; APPLICANT: Jiang, Bo
 ; APPLICANT: Boone, Charles
 ; APPLICANT: Bussey, Howard
 ; TITLE OF INVENTION: Nucleic Acids Encoding Anti-fungal Drug Targets and Methods of
 ; FILE OF INVENTION: Use
 ; CURRENT APPLICATION NUMBER: US/10/741,849
 ; PRIORITY FILING DATE: 2003-12-19
 ; PRIOR APPLICATION NUMBER: US 60/434,832
 ; PRIORITY FILING DATE: 2002-12-19
 ; NUMBER OF SEQ ID NOS: 8000
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 6021
 ; LENGTH: 2259
 ; TYPE: DNA
 ; ORGANISM: Candida albicans
 US-10-741-849-6021

Alignment Scores:
 Pred. No.: 3,81e-99 Length: 2259
 Score: 891.00 Matches: 229
 Percent Similarity: 46.6% Conservative: 98
 Best Local Similarity: 32.7% Mismatches: 232
 Query Match: 25.7% Indels: 142
 DB: 8 Gaps: 21

US-10-620-914-45 (1-648) x US-10-741-849-6021 (1-2259)

Qy 172 GlyLeuValGlyValAlaAaspPheTyrValSer-----GlyLysTyr 185
 Db 628 GGTATTATTGCACTGTGGATTTTTGGTATTCAAAAGCAGTGACACCTCAATGCGTATC 687
 Qy 186 Asp-----LeuProLeuArgGlnMetProTyrSerArgArgPhePheTyrArg 201
 Db 688 AATACTGTTGGTGGTGGTTAAACAGGACAACTCTTGGAATATTACGTAATTTTGGAGA 747
 Qy 202 SerIlePheAspIleAspAsnIleAspGlyProGluArgAlaTyrLeuGluGln 221
 Db 748 ATTTGGTTTGAAGCTGATAAAGTGTCTTTGGATCTTCAAGAGAACAATATTGGAAAT 807
 Qy 222 LysLeuGluArgValTyrGluGlnAsnThrGln-----GlySerIleProTyr 237
 Db 808 AAATTTGGTACCGTCAAAATCTTTGAATTCATACCAAGGCGCTTTGGGTAATAATC----- 861
 Qy 238 ValProTyrLeuArgAlaProTyrTyrValTyrIleGlyArgLeuProSerValGlyHis 257
 Db 862 -----CCCTATTATTATTTGGATTGGTTGTGATAAATCAAAATCACAC 903
 Qy 258 AlaLeuHisGluGlu-----ArgValGluArgProPrometPheProProThr 273
 Db 904 ACCATTTTGAAGAGATTGAATTTGTAGCCACTGAATCCCTTACCTTGCTCCAACATACA 963
 Qy 273 ----- 273
 Db 964 ACTCCAATCGCTAATCAACTTGAAGATATTCCAATTTTCTAAAGGTCATGAAGCTGCTTTA 1023
 Qy 273 ----- 273
 Db 1024 ATCAACTTGCNAAAAAAATTTACCTTACCCTCAATGTACTATCAAAAGGAATATTGGAGA 1083
 Qy 274 -----PheLeuTyrThr 277
 Db 1084 GTCTACTATGATGAATGAATCCATTCTGTATGAACAATTTTAAACCAATACATTATGCT 1143
 Qy 278 GlnSerTyrGluAspProGluProAspMetGluValMetGluIleAsnProLysAspThr 297
 Db 1144 TTCACTTGGGAAGATCCTCGTGAAGATCATAAACTTTTGAATTTTACCAGTGATGATACT 1203
 Qy 298 ValLeuThrLeuThrSerGlyGlyCysAsnAlaLeuAsnLeu-----LeuValGlnGly 315
 Db 1204 GTTTTGCTATTACTTCAGCTGGTGATATAATTTTGATGTATGTAGTTACCAACACCA 1263
 Qy 316 AlaGlyGlnValValSerValAspCysAsnProAlaGlnSerAlaLeuLeuGluLeuLys 335
 Db 1264 CCAAAAAGATTCATGCTGTTGATCTTAATCCATGTCAAAACCACTTTATTAGAATTGAAA 1323
 Qy 336 LysValAlaIleGlnGlnLeuGluPheGluAspValTyrGlnLeuPheGlyGlyGlyVal 355
 Db 1324 TTGGCTAGTTTGTAGATGCTTTCTCAAGAACAATTTGGTCAATTTGGTGAAGGTAAA 1383
 Qy 356 HisProArgIleGluGluLeuTyrGluLysLeuAlaProPheLeuSerGlnThrSer 375
 Db 1384 ATCGAAAATTTCAATGATCTTTTGATTGATCTTTTGGACCGCACATGCTCTTAATGCC 1443
 Qy 376 HisAsnPheTyrSerLysArg-----LeuTyrPheGlnHisGlyLeuTyrTyrGln 393
 Db 1444 TTCCAATACCTGGATGATGAAGGACCTTAAACCTTTTCTGGTAAAGGCTCTTAT----- 1497
 Qy 394 GlyGlyMetGlyLysLeuCysTyrValLeuGlnCys-----LeuAlaValValLeu 410
 Db 1498 ---GATACCTGGGTTTCTAGATGGCATTAAGATATTCAAGATATGTTTCAAAAGTTGC 1554
 Qy 411 GlyLeuGlyLysThrValLysArgLeuAlaAsnAlaProThrMetGluGluGlnArgArg 430
 Db 1555 GGTGTTAGTAAATACGTTGAAGAACTTTGTGCTCAACCACTGGAAGAACAATTTGAGA 1614
 Qy 431 LeuTyrAspSerAsnMetLeuIleHisPheValLysAsnGlyProLysValTyr 450
 Db 1615 ATTTGGAATGAACATTG-----AAACCAACT----- 1641
 Qy 451 LeuPheValLysPheVal---SerLeuValLeuPheAsnLysAlaValLeuTyrPheGly 469

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Db 1642 TTAATTAATCTGTGGTGGTTCATCTGTTGGTAATCAATGTTTATGGAAGCT 1701
||||| ||| ||||| : : : ||| |||||
Qy 470 GlyGlyValProGlyLysGlnTyrAlaLeuLeuLysAlaAspGlyIleProIleGluAsn 489
||||| ||||| : : : ||||| : : : |||||
Db 1702 TTGGAGTTCAGCTAATCAAGCAGCTTTAATG-----GGACCATCTGTTATTAAA 1752
||||| ||||| : : : ||||| : : : |||||
Qy 490 TyrIleAlaArgThrMetAspGlyValAlaGluAsnSerHisValArgLysGlnAsnTyr 509
||||| ||||| : : : ||||| : : : |||||
Db 1753 TATGTTGTGTACTTTGGACCAATCATTAAGAGATCGATGATTTCAATGATAACTAT 1812
||||| ||||| : : : ||||| : : : |||||
Qy 510 PheTyrTyrAsnCysLeuThrGlyLysPheLeuArgAspAsnCysProThrTyrLeuArg 529
||||| ||||| : : : ||||| : : : |||||
Db 1813 TTCTACTATTATGATGATGGGAGATACACCAAAAACAATTTGCCAGATTATTAACT 1872
||||| ||||| : : : ||||| : : : |||||
Qy 530 GluAlaAlaPheAlaThrLeuLys-----SerGlyValVal 541
||||| ||||| : : : ||||| : : : |||||
Db 1873 ACAAAAGGTTTCAACAGATTATCTAGCACCTGCTACTGCCAGCGGATCATCTCCAATT 1932
||||| ||||| : : : ||||| : : : |||||
Qy 542 AsnLeuThrValSerThrAsnPheMetGlu-----GluLeuLysAlaArg 558
||||| ||||| : : : ||||| : : : |||||
Db 1933 GACAACCTTAGAATCCACACTGACACTTTAAATGAAGTGTGTTGGTAGATTAAAGAAAAA 1992
||||| ||||| : : : ||||| : : : |||||
Qy 559 ThrTyrThrLysValIleLeuMetAspHisValAspTyrLeuAsp-----MetPro 575
||||| ||||| : : : ||||| : : : |||||
Db 1993 TCAATCACTATTGCCATTATCATGGATCATATGATGTTGGTTGACCTTAATGTTAGAT 2052
||||| ||||| : : : ||||| : : : |||||
Qy 576 ValAlaAsnGluLeuAlaGluCysLeuAlaLysGlnValAlaProGlyGlyIleValIle 595
||||| ||||| : : : ||||| : : : |||||
Db 2053 GCTATTAAATGAATTTACT--GCTTTGAAAAAGATGCTTTGCCAGGGGGTAGAGTATTA 2109
||||| ||||| : : : ||||| : : : |||||
Qy 596 TrpArgSerAlaSerLeuSerProProTyrAlaGluLeuIleGlnLysAlaGlyPhe--- 614
||||| ||||| : : : ||||| : : : |||||
Db 2110 CTTAGATCAGCAAGTACAAAGCCTTGGTACTTTGAAAAATTCAAGAACTTGGGATTCCAA 2169
||||| ||||| : : : ||||| : : : |||||
Qy 615 AspValArgCysIleArgAlaAlaThrGlnGlyTyrMetAspArgValAsnMetTyrSer 634
||||| ||||| : : : ||||| : : : |||||
Db 2170 GAAGAGAAAATGTTGTTGTCGAACCTGTTCAAGTATAGACAGAGTTAATATGATGCC 2229
||||| ||||| : : : ||||| : : : |||||
Qy 635 Ser 635
: : :
Db 2230 AAT 2232
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RESULT 4

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US-10-620-914-49
; Sequence 49, Application US/10620914
; Publication No. US20040093639A1
; GENERAL INFORMATION:
; APPLICANT: Benning, Christoph
; APPLICANT: Riekhof, Wayne
; APPLICANT: Klug, Rouven
; TITLE OF INVENTION: Compositions and Methods for the Production of Betaine Lipids
; FILE REFERENCE: MSU-07769
; CURRENT APPLICATION NUMBER: US/10/620,914
; CURRENT FILING DATE: 2003-07-16
; PRIOR APPLICATION NUMBER: 10/118,495
; PRIOR FILING DATE: 2002-04-08
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 49
; LENGTH: 2727
; TYPE: DNA
; ORGANISM: Neurospora crassa
US-10-620-914-49
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Alignment Scores:
Pred. No.: 5, 71e-94 Length: 2727
Score: 850.50 Matches: 239
Percent Similarity: 44.4% Conservative: 109
Best Local Similarity: 30.5% Mismatches: 240
Query Match: 24.6% Indels: 198
DB: 7 Gaps: 23
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US-10-620-914-45 (1-648) x US-10-620-914-49 (1-2727)
Qy 19 LeuGluLysLeuLysLeuSerSerMetLysAspSerLeuThrValLeuArgHisMet--- 37
||||| : : : ||||| : : : ||||| : : : |||||
Db 449 TTGAGGAGCTGGAGATG---GGCTTGAAAAAGACAAAGGAATGGGAAGACATGTGTAA 505
||||| : : : ||||| : : : ||||| : : : |||||
Qy 38 --TrpPheGlySerLysLysGlyAspHisAlaAlaArgLeuGluSerPheTyrGly 56
||||| ||||| : : : ||||| : : : |||||
Db 506 CCGTGGCGGGACAG-----GGA 523
||||| : : : ||||| : : : |||||
Qy 57 ProGlnAlaAlaPheAlaAlaArgLeuAlaGluArgSerAsnLeuIleTrpValAsp 76
||||| : : : ||||| : : : ||||| : : : |||||
Db 524 CCG-----GCACAAGGAGGAAACCG-ATATGGGTAGAT 555
||||| : : : ||||| : : : |||||
Qy 77 LeuGlyGlyThrGlyGluAsnValAspMetMetAlaAspTyrIleAspLeuAlaLys 96
||||| : : : ||||| : : : ||||| : : : |||||
Db 556 GTCGTTGGGGCACAGGCTGGAATATCGAACCCATGGCCAAAGTTGTCAACGCTCTCTCAA 615
||||| : : : ||||| : : : ||||| : : : |||||
Qy 97 ---PheLysSerIleTyrValValAspLeuCysHisSerLeuCysGluValAlaLysLys 115
||||| : : : ||||| : : : ||||| : : : |||||
Db 616 TTCTTCAAGACTGTTTACCTAGTGGACTTTTCGGCGTCACCTTTGTGAAGTGGCTAGGAAG 675
||||| : : : ||||| : : : ||||| : : : |||||
Qy 116 LysAlaLysAlaLysGlyTyrLysAsnValGlnValValGluAlaAspAlaCysGlnPhe 135
||||| : : : ||||| : : : ||||| : : : |||||
Db 676 CGGTTTGCAGGCTGGGTGGGAGAAATGTGAGAGTTATCTGCACGGATGCTCGCAAGTTT 735
||||| : : : ||||| : : : ||||| : : : |||||
Qy 136 Ala-----ProProGluGlyThr----- 141
||||| : : : ||||| : : : |||||
Db 736 AGGCTTGAGGATTATGAGGATGTTGACGAAGAGAGAGTCTGGCTCTGGAGATTCTTCGGCT 795
||||| : : : ||||| : : : ||||| : : : |||||
Qy 142 -----AlaThrLeuIle 145
||||| : : : ||||| : : : ||||| : : : |||||
Db 796 TCTTTGTCGGTGGTGGGGGAGACGAGCGGGGACACATCGCGGAGCTGAGTTGATC 855
||||| : : : ||||| : : : ||||| : : : |||||
Qy 146 ThrPheSerTyrSerLeuThrMetIleProProPheHisAsnValIleAspGlnAlaCys 165
||||| : : : ||||| : : : ||||| : : : |||||
Db 856 ACCATGCTTATAGCTTTCGATGATGCGGATATTATTTCTCGATTATGATTCGCTCGAG 915
||||| : : : ||||| : : : ||||| : : : |||||
Qy 166 SerTyrLeuSerGlnAspGlyLeuValGlyValAlaAspPheTyrValSerGlyLysTyr 185
||||| : : : ||||| : : : ||||| : : : |||||
Db 916 TCTCTGTTAGCACCTCAGCGGCTTGATTGCGCTCGTGGACTTTTACGCCAGTCGAAAGTC 975
||||| : : : ||||| : : : ||||| : : : |||||
Qy 186 Asp-----LeuProLeuArgGlnMetProTyrSerArg 196
||||| : : : ||||| : : : ||||| : : : |||||
Db 976 GACTTCACATTCGCACTACACGGTGGTCTTATGAACCCGACACAGTTGGCTATTTCGCG 1035
||||| : : : ||||| : : : ||||| : : : |||||
Qy 197 ArgPhePheTrpArgSerIlePheAspIleAspAsnIleAspIleGlyProGluArgArg 216
||||| : : : ||||| : : : ||||| : : : |||||
Db 1036 CGGAACCTTCTGGCGCTCGTGGTTCGATGCTGACAGGGTGTCTCTTGAGCCAGCTCGTCCA 1095
||||| : : : ||||| : : : ||||| : : : |||||
Qy 217 AlaTyrLeuGluGlnLysLeuGluArgValTrp-----GluGlnAsnThrGln 232
||||| : : : ||||| : : : ||||| : : : |||||
Db 1096 GATTATCTCGAGTACAGGTTTCGGGACTGCTCTGACCCGTCACCCGCAACACACTTTG 1155
||||| : : : ||||| : : : ||||| : : : |||||
Qy 233 GlySerIleProTyrValProTyrLeuArgAlaPro-----TyrTyrVal--- 247
||||| : : : ||||| : : : ||||| : : : |||||
Db 1156 GGAGCAATTCCTTACTACATCTGGTTGGG-ATGCTCTCAAGAAGCCCTTTCTTACGTCGAG 1214
||||| : : : ||||| : : : ||||| : : : |||||
Qy 248 -----TrpIleGlyArgLeuPro----- 253
||||| : : : ||||| : : : ||||| : : : |||||
Db 1215 TCTACCACACGAAATTTGTGAACACATCATCGATGCTATTTCGACAGAGATCCCCAAGATCATC 1274
||||| : : : ||||| : : : ||||| : : : |||||
Qy 253 ----- 253
||||| : : : ||||| : : : ||||| : : : |||||
Db 1275 ACCCGCTCTAGTGGGCAAAACATTCTTCTCTAGCAACAAATGGCGTAGGCTTTGCGTCGG 1334
||||| : : : ||||| : : : ||||| : : : |||||
Qy 254 -----SerValGlyHisAlaLeu-----HisGluGluArgValGlu 265
||||| : : : ||||| : : : ||||| : : : |||||
Db 1335 CCGCACACGCGCGGAGATGCGCTCAAGGCCCTTCAATACGGCCATCGAGACATCTCGGC 1394
||||| : : : ||||| : : : ||||| : : : |||||
Qy 266 ArgPro-ProMet----- 269
||||| : : : ||||| : : : ||||| : : : |||||
Db 1395 CAACCTACTCTCTCCCGTCCTTCTTCTACAAAATCACCACCTGGAGGATCTACTACGACGA 1454
||||| : : : ||||| : : : ||||| : : : |||||
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QY 270 -----PheProThrPheLeuTyThrGlnSerTrpGluAs 282
Db 1455 TCAACTCCCGAAGCACACCCAGTTCAATGACGAGTACATCTACGCTTTTACCTGGGAAGA 1514
QY 282 pProGluProAspMetGluValMetGluLeuLeuLeuLeuLeuLeuLeuLeuLeuTh 302
Db 1515 CTCGGCGTGCAGAGAGAACTCTTAACCTCCGGGCCGAGCGTCTCTAGCCATCAC 1574
QY 302 rSerGlyGlyCysAsnAlaLeuAsnLeuLeuValGlnGlyAlaGlyGlnValValSerVa 322
Db 1575 CAGCGCGGCGCAACATCTTCTTCTACCTGATGACAGTCCCGCTCGGCTCACGCCAT 1634
QY 322 lAspCysAsnProAlaGlnSerAlaLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 342
Db 1635 CGACCTAAACCCAGCCCAACACCTGCTTCAAACTCAAAGTCGCTCTTTTACGACTCT 1694
QY 342 ucluPheGluAspValTrpGlnLeuPheGlyGluGlyValHisProArgIleGluGluLe 362
Db 1695 GGAATTAACCCGACGCTTGGAGATCTTCGGTGAGGCAACACCCCGACTTTTCGCTCACT 1754
QY 362 uTyrgLulysLysLeuAlaProPheLeuSerGlnThrSerHisAsnPheTrpSerLysAr 382
Db 1755 GCTCATCTCCAACCTCTCCCTCACCTCCGCGCGGCTTCACTACTGCTATCCAA 1814
QY 382 gLeuTrpTyrrPheGln-----HisGlyLeuTyrrGlnGlyGlyMetGlyLy 398
Db 1815 TGCGCACATATTTCGACACCTCGCGGGCGGCTCTCTATGATACCGCGGCTCCGATA 1874
QY 398 sLeuCystrpValLeuGlnCysLeuAlaValValLeuGlyLeuGlyLysThrValLysAr 418
Db 1875 CGCTATCGGTTTCTCCGCTGGATTTCCACACTCTTCTTCGCGCTCCGCGCTCCGTCG 1934
QY 418 gLeuAlaAsnAlaProThrMetGluGluGlnArgLeuTrpAspSerAsnMetLeu1l 438
Db 1935 ACTTCTCTACTCTCCACCTCGAAGGCAAGTTCCATCTACACACCAAGATT----- 1989
QY 438 eHisPheValLysAsnGlyProLeuValTrpLeuPheValLysPheValSer-- 457
Db 1990 -----CGTCCCTGT-----CTGCTCAACCGCTTCTGTCACCGG 2021
QY 458 -leuValLeuPheAsnLysAlaValLeuTrpPheGlyGlyGlyValProGlyLysGlnTy 477
Db 2022 CTGTGCTCTCAGCTCCGACGCTTCTCTGTGCGGCTTGTGGCGTGCCCAAGATCAAGT 2081
QY 477 rAlaLeuIleLysAlaAsp----- 483
Db 2082 GGTATGATCGAGCGGACTACCAACCGGCTTCTATCTCTCTCCACCCACCCCGAG 2141
QY 484 -----GlyIleProileGluAsnTyrrIleAlaArgThrMetAspGl 497
Db 2142 CAAGAAAAAACCAGCGCGCGGAAGCAATCTCCACTACACAACTCCACCTTGATCC 2201
QY 497 yValAlaGluAsnSerHisValArgLysGlnAsnTyrrPheTyrrAsnCysLeuThGl 517
Db 2202 CGTCTCTCCACCTCCCACTTCGCTCGGCAACCCCTTACTACTCTGCTGTGCTCGG 2261
QY 517 yLysPheLeuArgAspAsnCysProThrTyrrLeuArgGluAlaAlaPheAlaThrLeuLy 537
Db 2262 ACAATACACGCCAGTGCATCCGATTAACCTTCCCTCCGCGCCACTCTATACTCAG 2321
QY 537 sSer---GlyValValAspAsnLeuThrValSerThrAsnPhePheMetGluGluLeu-- 555
Db 2322 CGCTCCTGGAGCTTTGACGGCTTACGCATCCACACGATGAATAACAGGAGGTGTTGGC 2381
QY 556 -----LysAlaArgThrTyrrLysValIleLeuMetAspHisValAspTrpLeuAs 573
Db 2382 TAGGTTTCAGCGGGTACTTTGACAGTAGCGGTGATGATAGTAGTAGTGTGTTGCTCA 2441
QY 573 pMetPro-----ValAlaAsnGluLeuAlaGluCy 583
Db 2442 TCCGCTTCCGCTGAGGAGGAAAGGAAGGAGGCGGAGGAGGAGGAGGAGGAGGAG 2501
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QY 583 sLeuAlaLysGlnValAlaProGlyGlyIleValIleTrpArgSerAlaSerLeuSerPr 603
Db 2502 GTTGAATCGGCGGTTGAAGGTGGAAGGTGTTGTTGAGAGCGCGGAGTGGAGCC 2561
QY 603 oProTyrrAlaGluLeuIleGlnLysAlaGlyPheAspValArgCysAlle----- 619
Db 2562 GTGGTATGTAGGGGTTTTTGTGAGGAAGGGTTTGAGCAGAGAGGTGGTGGTTCGTGA 2621
QY 620 ----ArgArgAlaThrGlnGlyTyrrMetAspArgValAsnMetTyrrSerSerPheTyrrMe 638
Db 2622 ATCCGGAAGGGGGGACAGGAGTGTATTGACAGGGTGAATATGTATGCTAGTTGTTGGAT 2681
QY 638 tAlaArgArg 641
Db 2682 CTTGGAAG 2691
RESULT 5
US-10-620-914-48
; Sequence 48, Application US/10620914
; Publication No. US20040093639A1
; GENERAL INFORMATION:
; APPLICANT: Benning, Christoph
; APPLICANT: Riekhof, Wayne
; APPLICANT: Klug, Rouven
; TITLE OF INVENTION: Compositions and Methods for the Production of Betaine Lipids
; FILE REFERENCE: MSU-07769
; CURRENT APPLICATION NUMBER: US/10/620,914
; CURRENT FILING DATE: 2003-07-16
; PRIOR APPLICATION NUMBER: 10/118,495
; PRIOR FILING DATE: 2002-04-08
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 48
; LENGTH: 3427
; TYPE: DNA
; ORGANISM: Neurospora crassa
US-10-620-914-48
Alignment Scores:
Pred. No.: 5,11e-88 Length: 3427
Score: 804.00 Matches: 238
Percent Similarity: 43.2% Conservative: 112
Best Local Similarity: 29.4% Mismatches: 256
Query Match: 23.2% Indels: 205
DB: 7 Gaps: 24
US-10-620-914-45 (1-648) x US-10-620-914-48 (1-3427)
QY 19 LeuGluLysLysLysLeuSerSerMetLysAspLeuThrValLeuArgHisMet--- 37
Db 776 TTGGAGGAGCTGGAGATG---GGCTTGAATAAAGACAAAGGAATGGGAAGACATGTGTAA 832
QY 38 ---TrpPheGlySerLysLysGlyAspAspHisAlaAlaArgLeuGluSerPheTyrrGly 56
Db 833 CCGTGCCGCGGACAGGACCGGACCAAGGA-----GGAAACCGATATGGG 877
QY 57 ProGlnAlaAlaAlaPheAlaArgLeuAla-----GluArgSerAsn 71
Db 878 TAGATGTACGCTCTCATCAGAACCTTGCATTTGGAATCCACACAGCGGTGACC 937
QY 72 LeuIleTrpValAspLeuGlyGlyGlyThrGlyGluAsnValAspMetMetAlaAspTyrr 91
Db 938 ATCGCTACAAAACACAGTCCGTGGGGGCACAGCTGGAATATCGAAGCATATGCCAAGTTT 997
QY 92 IleAspLeuAlaLys---PheLysSerIleTyrrValValAspLeuCysHisSerLeuCy 110
Db 998 GTCACGCTCTGTAATCTTCAAGACTGTTTACCTAGTGGACTTTTCGCCGCTCACTTGT 1057
QY 111 GluValAlaLysLysLysAlaLysAlaLysGlyTyrrLysAsnValGlnValGluAla 130
Db 1058 GAAGTGGCTAGGAAGCGGTTTCCAGCGGTGGGGAGAAATGTGAGAGTATCTGCACG 1117
QY 131 AspAlaCysGlnPheAla-----ProProGluGlyThr----- 141
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; APPLICANT: Klug, Rouven
 ; TITLE OF INVENTION: Compositions and Methods for the Production of Betaine Lipids
 ; FILE REFERENCE: MSU-06897
 ; CURRENT APPLICATION NUMBER: US/10/118,495
 ; CURRENT FILING DATE: 2002-04-08
 ; PRIOR APPLICATION NUMBER: 60/283,812
 ; PRIOR FILING DATE: 2001-04-13
 ; NUMBER OF SEQ ID NOS: 42
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 1
 ; LENGTH: 1252
 ; TYPE: DNA
 ; ORGANISM: Rhodobacter sphaeroides
 US-10-118-495-1

Alignment Scores:
 Pred. No.: 7,19e-36 Length: 1252
 Score: 379.50 Matches: 127
 Percent Similarity: 43.1% Conservative: 68
 Best Local Similarity: 28.1% Mismatches: 182
 Query Match: 11.0% Indels: 75
 DB: 5 Gaps: 20

US-10-620-914-45 (1-648) x US-10-118-495-1 (1-1252)

Qy 231 ThrGlnGlySerIleProTyrValProThrLeuArgAlaProTyrTyrValTrpIleGly 250
 Db 4 ACGAGTTCGCCCTCACCCAGCTGCC-----GCCCGCGC-----GTTGCC 45
 Qy 251 ArgLeuProSerValGlyHisAlaLeuHis-----GluGluArg 263
 Db 46 CGC-----CAGATCGGCGCGCGCTGCACCGCAGCTTCCTCAGCGCGCAGGACTG 99
 Qy 264 ValGluArgProMetPheProThrPhe-----LeuTyrThrGlnSerTrp 280
 Db 100 ATGAGCGG-----ATGTTCTCGCGCTCTTCACGCGCTCGTCTATCCGAGATCTGG 153
 Qy 281 GluAspProGluProAspMetGluValMetGluIleAsnProLysAspThrValLeuThr 300
 Db 154 GAGGATCGCGCGGTGGACATCGCGCGCTCGCCATCTCGCCCGCGGACCGGTGGTGGCC 213
 Qy 301 LeuThrSerGlyGlyCysAsnAlaLeuValGlnGlnGlyAlaGlyGlnValVal 320
 Db 214 ATCGCTCGGCGGTTCGAACTGCTTTCTATCTCAGCAGCGGCGCGGTCTCATCTC 273
 Qy 321 SerValAspCysAsnProAlaGlnSerAlaLeuLeuGluLeuLysLysValAlaIleGln 340
 Db 274 GCGGTGATCTTCGCCCGCCCATCTGCGCTGGCGCGCTGAGCTCGCGCGCGCGG 333
 Qy 341 GlnLeu-----GluPheGluAspValTrpGlnLeuPheGlyGluGlyValHisProArgIle 359
 Db 334 ACGTCTGCCGACCATGCGCGCTTCTTCGATCTCTTCGGTTCGCGGACCTGCGCGCAAT 393
 Qy 360 GluGluLeuTyrGluLysLysLeuAlaProPheIleuSerGlnThrSerHisAsnPheTrp 379
 Db 394 CGCGCCCTCTACGACCGCCATCGCGCGCGCTCGACCGCGCGCGCGCGCTACTGG 453
 Qy 380 -----SerLysArgLeuTyrPheGlnHisGlyLeuTyrTyrGln 393
 Db 454 GAGGCGCGCAGCCCTTCGCGCGCGCATCTCAGCTGTTTCGAGCGCGGTCTTACCGGCAC 513
 Qy 394 GlyGlyMetGlyLysLysCysTrpValLeuGlnCysLeuAlaValValLeuGlyLeuGly 413
 Db 514 GGTGCCCTCGCGCGCTTCATCGCGCGCGCCCATACGCTCGCG-----CGGCGCGCGGCG 567
 Qy 414 LysThrValLysArgLeuAlaAsnAlaProThrMetGluGluGlnArgArgLeuTrpAsp 433
 Db 568 ACCGACCTCGCGCGCTTTCCTCAGTGTCCGACATCGAGGCGCGCGCGCTTCTTCTAC 627
 Qy 434 SerAsnMetLeuIleHisPheValLysAsnGlyProLysProLeuValTrpLeuPheVal 453
 Db 628 GCCCATATC-----GGGCG-----CTTTTCGAG 651

Qy 454 LysPheValSerLeuValLeuPheAsnLysAlaValLeuTrpPheGlyGlyValPro 473
 Db 652 GCGCCGCTGGTGCAGCGCTCGCCCGCGCGCGCGCTCTTCGGGTGGGATCCCG 711
 Qy 474 GlyLysGlnTyrAlaLeuIleLysAlaAspGly-----IleProIleGluAsn 489
 Db 712 CCGCGCAATATGCGCTTCTGCGGAGACGCGCGGACGCGCGCTGCTGCGCGTG----- 765
 Qy 490 TyrIleAlaArgThrMetAspGlyValAlaGluAsnSerHis----- 503
 Db 766 -----CTGCGCGCAGCGCTCCACCGCGCTGCTGTGACTTC 801
 Qy 504 ValArgLysGlnAsnTyrPheTyrTyrAsnCysLeuThrGlyLysPheLeuArgAspAsn 523
 Db 802 CCCCTGCGCGAAGTACTTCCGCTTCAGGCGCATCGCCCGCGCTATCCGCGCGCGCGC 861
 Qy 524 -----CysProThrThrLeuArgGluAlaPheAlaThrLeuLysSerGlyVal 540
 Db 862 GAGGCGCGCTGCGCCCTTCTGAAACCCAGCTTCGAGACCTGCGCGAGAAC----- 918
 Qy 541 ValAspAsnLeuThrValSerThrAsnPheMetGluGluLeuLysAlaArgThrTyr 560
 Db 919 CGCGCGCGGTGCAGATCGAGAACCGCAGCCTGACCGAGCGCTCGCGCGCGAACCCGAG 978
 Qy 561 ThrLysVal-----IleLeuMetAspHisValAspTrpLeuAspMetProValAla 577
 Db 979 GAGAGCATCCAGCGCTTCACCTGCTGATCGCAGGACTGATGACGACGCGCAGCTG 1038
 Qy 578 AsnGluLeuAlaGluCysLeuAlaLysGlnValAlaProGlyGlyIleValIleTrpArg 597
 Db 1039 ACCCGCTCTCGCGCGAGTGCAGCGCATCGCGCGCGCGCGCGGTGATCTTCGCG 1098
 Qy 598 -----SerAlaSerLeuSerProTyrAlaGluLeuIleGlnLysAlaGlyPhe 614
 Db 1099 ACCGCGCGCGCGCGCGCTGCTGCGC-----GCCCGAGTCCCGAGGAGATCTCGG 1152
 Qy 615 AspValArgCysIleArgArgAlaThrGlnGly-----TyrMetAspArgValAsnMet 632
 Db 1153 CACTGGCGATC 1212
 Qy 633 TyrSerSerPheTyrMetAlaArgLysGlyAla 644
 Db 1213 TACGCGCGCTTCCACCTCTACCGCGCGGAGGACGCC 1248

RESULT 7
 US-10-620-914-1
 ; Sequence 1, Application US/10620914
 ; Publication No. US20040093639A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Benning, Christoph
 ; APPLICANT: Riekhof, Wayne
 ; APPLICANT: Klug, Rouven
 ; TITLE OF INVENTION: Compositions and Methods for the Production of Betaine Lipids
 ; FILE REFERENCE: MSU-07769
 ; CURRENT APPLICATION NUMBER: US/10/620,914
 ; CURRENT FILING DATE: 2003-07-16
 ; PRIOR APPLICATION NUMBER: 10/118,495
 ; PRIOR FILING DATE: 2002-04-08
 ; NUMBER OF SEQ ID NOS: 52
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 1
 ; LENGTH: 1252
 ; TYPE: DNA
 ; ORGANISM: Rhodobacter sphaeroides
 US-10-620-914-1

Alignment Scores:
 Pred. No.: 7,19e-36 Length: 1252
 Score: 379.50 Matches: 127
 Percent Similarity: 43.1% Conservative: 68
 Best Local Similarity: 28.1% Mismatches: 182
 Query Match: 11.0% Indels: 75
 DB: 5 Gaps: 20


```

Qy 345 u---AspValTrpGlnLeuPheGlyGluGlyValHisProArgIleGluGluLeuTyrG1 364
Db : |||:||||: - |||||
342 GGGCGATGTTCCGCTTTTTCGGCGCGCCGACACACCGCCATTCGCAAGCCTATGA 401
Qy uLysLysLeuAlaProPheLeuSerGlnThrSerHisAsnPheTrpSerLysArgLeuTr 384
Db : |||:||||: - |||||
402 CCGCTTTATGCGCGCATCTCGATCCGTCAGCCGCCCATATTCGGAGCCGCCGAATG 461
Qy 384 p-----TyrPheGlnHisGlyLeuTyrTrpGlnGlyMetG1 397
Db : |||:||||: - |||||
462 GCGTGTGCGCGGCATCGCGCTCTTCGCGCAATTTCTACACGACCGCGCTCTCGG 521
Qy 397 YLysLeuCysTrpValLeuGlnCysLeuAlaValValLeuGly----- 411
Db : |||:||||: - |||||
522 C-----CTGTTTCATCGCCATGGCCATCGCACCGCGCAAAATT 557
Qy 412 -LeuGlyLysThrValLysArgLeuAlaAsnAlaProThrMetGluGlnArgArgLe 431
Db : |||:||||: - |||||
558 CTTCCGCGTCAACCGCGCCCATATGTAAGACCGAGGAATATCGCGAGCGCGCTT 617
Qy 431 uTrpAspSerAsnMetLeuIleHisPheValLysAsnGlyProLysProLeuValTrpLe 451
Db : |||:||||: - |||||
618 CTTCAACGAGGAGCTGGCGCGCTCTTCGACAG-----AAGCTTTTGAATGGC 668
Qy 451 uPheValLysPheValSerLeuValLeuPheAsnLysAlaValLeuTrpPheGlyG1 471
Db : |||:||||: - |||||
669 GACCTCGCGTAAGGCTCGCTG-----TTCCGCGCTCGG 701
Qy 471 YValProGlyLysGlnTyr-----AlaLeuIleLysAlaAspGlyIleProIleGluAs 489
Db : |||:||||: - |||||
702 CATTCCGCGCGCGAGTAGATTCCTGATCCTTCAGCGACGCGCACCATGGCGAGCGT 761
Qy 489 nTyrIleAlaArg-----ThrMetAspGlyValAlaGluAsnSerHisValar 505
Db : |||:||||: - |||||
762 TCTGAAGCCCGCGTGGAAAGCTCGCTCGATTTTCCCTGGAAAC----- 810
Qy 505 gLysGlnAsnTyrPheTyrTrpAsnCysLeuThrGlyLysPheLeuArgAspAsn----- 523
Db : |||:||||: - |||||
811 -----AATTATTTCGCTCGAGGCTTTTCGCGCGCGCTATCCAAATCCCGTGAGGC 863
Qy 524 ---CysProThrTyrLeuArgGluAlaAlaPheAlaThrLeuLysSerGlyValValas 542
Db : |||:||||: - |||||
864 CGCCCTGCGCCCTATCTGGAAGAACAGAACTAGCAAAACCATCCG-----GGCAATATCGA 920
Qy 542 pAsnLeuThrValSerThrAsnPhePheMetGluGluLeu-----LysAlaArgTh 559
Db : |||:||||: - |||||
921 CCGGTGCGCATCCACCATGCAATCTGATCGAATTCCTCGCGCAGGAGCGGGCAC 980
Qy 559 rTyrThrLysValIleLeuMetAspHisValAspTrpLeuAspMetProValAlaAsnG1 579
Db : |||:||||: - |||||
981 CGTCGATCGCTTCATCTCTGCTCGATGCGCAGGACTGGATGACCGATGACCAAGCTCAACGC 1040
Qy 579 uLeuAlaGluCysLeuAlaLysGlnValAlaProGlyGlyIleValIleTrpArgSerAl 599
Db : |||:||||: - |||||
1041 GCTGTGTGCGAAATCAGCCGACCGCTCGCGAGCGCGCGCTCATCTTCGCGCGC 1100
Qy 599 a-----SerLeuSerProTyrAlaGluLeuIleGlnLysAlaGlyPheAsp-V 616
Db : |||:||||: - |||||
1101 CGCGAGCCGAGCTGTGCGCAGCGCGCTCTGACCTCGCTGCTCGACCATGGGACTA 1160
Qy 616 alArgCysIleArgArgAlaThrGlnGlyTyrMetAspArgValAsnMetTyrSerSerp 636
Db : |||:||||: - |||||
1161 TCAGGACGAGGCGTCCGCGCAATCTTCGCGACGC-GACCGTTCGCGCATCTATGCGCGCT 1219
Qy 636 heTyrMetAlaArgLysGlyAla 644
Db : |||:||||: - |||||
1220 TCCACCTCTATGTGAAGCGCACGGCA 1245

```

RESULT 9

US-10-620-914-22

; Sequence 22, Application US/10620914

; Publication No. US20040093639A1

GENERAL INFORMATION:

```

; APPLICANT: Benning, Christoph
; APPLICANT: Riekhof, Wayne
; APPLICANT: Klug, Rouven
; TITLE OF INVENTION: Compositions and Methods for the Production of Betaine Lipids
; FILE REFERENCE: MSU-07769
; CURRENT APPLICATION NUMBER: US/10/620,914
; PRIOR FILING DATE: 2003-07-16
; PRIOR FILING DATE: 2002-04-08
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 22
; LENGTH: 1248
; TYPE: DNA
; ORGANISM: Mesorhizobium loti
US-10-620-914-22

```

Alignment Scores:

```

Pred. No.: 1,39e-29 Length: 1248
Score: 329.00 Matches: 118
Percent Similarity: 42.8% Conservative: 66
Best Local Similarity: 27.4% Mismatches: 184
Query Match: 9.5% Indels: 63
DB: 7 Gaps: 15

```

US-10-620-914-45 (1-648) x US-10-620-914-22 (1-1248)

```

Qy 248 TrpIleGlyArgLeuProSer-----ValGlyHisAlaLeuHisGluGluArgValGlu 265
Db : |||:||||: - |||||
48 TGGAAAGCGCGCTTACAGAACCGCGCGCTTCCAAAGCCGCGATCTCCGAGCGGCTGT 107
Qy 266 ArgProMetPheProPro-ThrPheLeuTyrThrGlnSerTrpGluAspProGluPr 285
Db : |||:||||: - |||||
108 GCGCTTCTGTTTTCGCGCTCGTC-----TATCCGCGATCTGGGAAGACCCGATGT 161
Qy 285 oAspMetGluValMetGluIleAsnProLysAspThrValLeuThrLeuThrSerGlyG1 305
Db : |||:||||: - |||||
162 CGACATCGAGGCCATCGAGCTTGTGTCAGGCGCATCGCATCGTCAATCGCTTCGCGGG 221
Qy 305 YCysAsnAlaLeuAsnLeuValGlnGlyAlaGlyGlnValSerValAspCysAs 325
Db : |||:||||: - |||||
222 CTGCAACATCTTCGCTACCTACCTCCGTCGCGCGCAGGATCGACGCGCTCGACCTCA 281
Qy 325 nProAlaGlnSerAlaLeuLeuGluLeuLysValAlaIleGlnGlnLeuGluPheG1 345
Db : |||:||||: - |||||
282 CGCGCGCCACATCGCGCTGAACCGCATGAAGCTGAGCGCGTGGCGCTCTGCCCTCGCA 341
Qy 345 u---AspValTrpGlnLeuPheGlyGluGlyValHisProArgIleGluGluLeuTyrG1 364
Db : |||:||||: - |||||
342 GGGCGATCTGTTCGCGCTTTTTCGCGCGCGCGCACACCGCCCAATTCGCAAGCCTATGA 401
Qy 364 uLysLysLeuAlaProPheLeuSerGlnThrSerHisAsnPheTrpSerLysArgLeuTr 384
Db : |||:||||: - |||||
402 CCGCTTTATGCGCGCATCTCGATCCGTCAGCGCGCGCCATTCATTCGGAGCGCGCAATG 461
Qy 384 p-----TyrPheGlnHisGlyLeuTyrTrpGlnGlyMetG1 397
Db : |||:||||: - |||||
462 GCGTGTGCGCGCGCATCGCGCTTTCGCGCAATTTCTACACGACCGCGCTCTCGG 521
Qy 397 YLysLeuCysTrpValLeuGlnCysLeuAlaValValLeuGly----- 411
Db : |||:||||: - |||||
522 C-----CTGTTTCATCGCCATGGCCATCGCACCGCGCAAAATT 557
Qy 412 -LeuGlyLysThrValLysArgLeuAlaAsnAlaProThrMetGluGlnArgArgLe 431
Db : |||:||||: - |||||
558 CTTCCGCGTCAACCGCGCCCATATGTAAGACCGAGGAATATCGCGAGCGCGCTT 617
Qy 431 uTrpAspSerAsnMetLeuIleHisPheValLysAsnGlyProLysProLeuValTrpLe 451
Db : |||:||||: - |||||
618 CTTCAACGAGGAGCTGGCGCGCTCTTCGACAG-----AAGCTTTTGAATGGC 668
Qy 451 uPheValLysPheValSerLeuValLeuPheAsnLysAlaValLeuTrpPheGlyGlyG1 471

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Db 669 GACCTCGGTAAAGCCTCGCTG-----TTTCGGCCCTCG 701
Qy 471 yValProGlyLysGlnTyr-----AlaLeuIleLysAlaAspGlyIleProIleGluAs 489
Db 702 CATTCGGCGGCGAGTACGATTCCCTGATCACCCTCAGGCGACGACCATGGCCAGCGT 761
Qy 489 nTyIleAlaArg-----ThrMetAspGlyValAlaGluAanSerHisValar 505
Db 762 TCTGAAGCCCGGCTGGAAAGCTCGCTGCGATTTTCCCTGGAAAC-----810
Qy 505 gLysGlnAsnTyRPhTyTyrAsnCysLeuThrGlyLysLeuArgAspAsn-----523
Db 811 -----AATTAATTTCGCTGGCAGGCTTTTCCCGCGCTATCCAAATCCGGTGAGGC 863
Qy 524 ----CysProThrTyRLeuArgGluAlaAlaPheAlaThrLeuLysSerGlyValValas 542
Db 864 CGCCTGCGCCCTATCTGGAAGAGCAGAACTACGAAACCATCCGC---GGCAATATCGA 920
Qy 542 pAsnLeuThrValSerThrAsnPhePheMetGluLleu-----LysAlaArgTh 559
Db 921 CCGGTGCGCCATCCACCATGCCAATCTGATCGAATTCCTCGCGGCAAGGACGCGGGCAC 980
Qy 559 rTyThrLysValIleLeuMetAspHisValAspTrpLeuAspMetProValAlaAsnG1 579
Db 981 CGTCGATCGCTTCATCTCTGCTGATGCCAGAGCTGGATGACCGATGACCATCCACGC 1040
Qy 579 uLeuAlaGluCysLeuAlaLysGlnValAlaProGlyGlyIleValIleTrpArgSerAl 599
Db 1041 CTTGTGTGGGAAATCAGCCGACCGCTCGCGCAGCGCGCGCTCATCTTCCGACCGC 1100
Qy 599 a-----SerLeuSerProTyRAlaGluLeuIleGlnLysAlaGlyPheAsp-V 616
Db 1101 GCGGAGCCCGAGCTGTGCGCAGGCGCGTCTCGACCTCGCTGCTCGACCATGTGGACTA 1160
Qy 616 alArgCysIleAlaArgAlaThrGlnGlyTyRMetAspArgValAsnMetTyRSerSerp 636
Db 1161 TCAGGACGAGCGTTCGCGGAAATCTTCGGCAGCG-GACCGTTCGGCCATCTATGGCGCT 1219

RESULT 10
US-10-118-495-28
; Sequence 28, Application US/10118495
; Publication No. US20030074688A1
; GENERAL INFORMATION:
; APPLICANT: Benning, Christoph
; APPLICANT: Riekhof, Wayne
; APPLICANT: Klug, Rouven
; TITLE OF INVENTION: Compositions and Methods for the Production of Betaine Lipids
; FILE REFERENCE: MSU-06897
; CURRENT APPLICATION NUMBER: US/10/118,495
; PRIOR FILING DATE: 2002-04-08
; PRIOR FILING DATE: 60/283,812
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 28
; LENGTH: 1251
; TYPE: DNA
; ORGANISM: Agrobacterium tumefaciens
US-10-118-495-28

Alignment Scores:
Pred. No.: 2,86e-29 Length: 1251
Score: 326.50 Matches: 115
Percent Similarity: 47.6% Conservative: 71
Best Local Similarity: 29.4% Mismatches: 162
Query Match: 9.4% Indels: 46
DB: 5 Gaps: 14
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US-10-620-914-45 (1-648) x US-10-118-495-28 (1-1251)
Qy 275 LeuTyRThrGlnSerTrpGluAspProGluProAspMetGluValMetGluIleAsnPro 294
Db 130 GTCTATCCGAGATCTCGGAAGACCCGAGATCGACATGGAAGCATGGAGCTTGGCGAA 189
Qy 295 LysAspThrValLeuThrSerGlyCysAsnAlaLeuAsnLeuValGln 314
Db 190 GCCCACCAGCATCGTACCATCGCTCGGCGGCTGCAACATGCTGGCTATCTCTCGCGC 249
Qy 315 GlyAlaGlyGlnValSerValAspCysAsnProAlaGlnSerAlaLeuGluLeu 334
Db 250 AACCCGCGCAGCATCGATGTGTGGAAGCTCAACCCGACCATCGCGCTCAACAAGCTG 309
Qy 335 LysLysValAlaIleGlnGlnLeu---GluPheGluAspValTrpGlnLeuPheGlyC1u 353
Db 310 AAGCTCGCTGCTTCCCGCATCTCCCGCCCATCAGGATGTGTGCGCATCTCGCGCGC 369
Qy 354 GlyValHisProArgIleGluGluLeu---TyRLeuLysLysLeuAlaProPheLeuSerG1 373
Db 370 GCCCG-CACCCGAGACAGCGTCGGTTATGACCGTTTCATCGCGAGCATCTGGATGC 428
Qy 373 nThrSerHisAsnPheTrpSerLys-----ArgLeuTyRTrpPh 386
Db 429 CACGACCAAGGCATACTGTGGAAGCGCACCTTTCCGGCGCGCTTCGATTTCCGTT 488
Qy 386 eGlnHisGlyLeuTyRTrpGlnGlyGlyMetGlyLysLeuCysTrpValLeuGlnCysLe 406
Db 489 CGACAGGAACATCTACCGGACCGCTCTCGCGCTTTCATCGCGCGCGGCACATCAT 548
Qy 406 uAlaValValLeuGlyLeuGlyLysThrValLysArgLeuAlaAsnAlaProThrMetG1 426
Db 549 GCCCGCTGACCGCGTGAACTCACC-----GAAATGCCAACACCGCGAGCTCGGA 602
Qy 426 uGluGlnArgLeuTrpAspSerAsnMetLeuIleHisPheValLysAsnGlyProLys 446
Db 603 CGAACAGCGCCAGTTTTTGTACAGCAGGTCGCGCGCTTTTC-----GACAA 650
Qy 446 sProLeuVal---TrpLeuPheValLysPheValSerLeuValLeuPheAsnLysAlaVa 465
Db 651 GCCCGTGTGCTGTGCTGACGAGCGCAAGCTCGCTT-----690
Qy 465 lLeuTrpPheGlyGlyValProGlyLysGlnTyr-----AlaLeuIleLysAl 482
Db 691 -----TTCCGCTTGGCATTCGCGCGCGCAGTATGACGAGCTGGCAAGCTTTCCAG 743
Qy 482 aAspGlyIleProIleGluAsnTyRLeuAlaArgThrMetAspGlyValAlaGluAsnSe 502
Db 744 CGACGCGC---ACGGTTGCTCCGTCCTCAAGGAGCGGCTGGAAAGCTTGGCTGCAACTT 800
Qy 502 rHisValArgLysGlnAsnTyRPhTyTyrAsnCysLeuThrGlyLysPheLeuArgAs 522
Db 801 CCCGCTC---AGCGACAATTAATTTCGCTGCGAGCGCTTTCGCGCGCTTATCCCGAGCC 857
Qy 522 pAsn-----CysProThrTyRLeuArgGluAlaAlaPheAlaThrLeuLysSerG1 539
Db 858 GCATCAGGCGTCCCTGCGCTTATCTCAAGCCGGAATATTACGAAAGATCCGCAACA 917
Qy 539 yValValAspAsnLeuThrValSerThrAsnPhePheMetGluGluLeuLys-----556
Db 918 CACCGCG---CGCGTTCGCGGTGCATCAGCCCATATACCGAGCTGCTTTCCCGCAAGCC 974
Qy 557 -AlaArgThrTyRThrLysValIleLeuMetAspHisValAspTrpLeuAspMetProVa 576
Db 975 GGCAATGGCGTCCAGCCGCTATATCTCTGATCGCGAGCTGGATGACGGATGTGCA 1034
Qy 576 lAlaAsnGluLeuAlaGluCysLeuAlaLysGlnValAlaProGlyGlyIleValIleTr 596
Db 1035 GCTCAACGAGTTATGGTCGAGATCAGCGCAGCTCCCGCATCCGGGCGCAGCGCTCATCTT 1094
Qy 596 pArgSerAlaSerLeu-----SerProTyRAlaGluLeuIleGlnLys 611
Db 1095 CCGCACCGCGCGCGA-AAAGAGCGTTATCGAGGCGCGCTTTTCGCGCGGACATCCGCAACC 1153
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Qy 373 GlnThrSerHisAsnPhetTrpSer-----LysArgLeuTrpTyr 385
Db 430 CCGCAACCCGCGCTATTGGAAACGGCCGAGATCTCACCGCGCGCGCGCATCGCGCTC 489
Qy 386 PheGlnHisGlyLeuTyrGlnGlyGlyMetGlyLysLeuCyeTyrValLeuGlnCys 405
Db 490 TTCGGCGCCAAAGTTTATCGTACCGCGCTGCTTGGCGGTTCATTTCGCCCGCAGCATGCT 549
Qy 406 LeuAlaValValLeuGlyLeuGlyLysThrValLysArgLeuAlaAsnAlaProThrMet 425
Db 550 CTCGACCGCTGCACGGCATCAATCCG-----GAAGATTTCGTCAAGCGCGCTCCATG 603
Qy 426 GluGlnGlnArgArgLeuTrpAspSerAsnMetLeuLeHisPheValLysAsnGlyPro 445
Db 604 CGCGAGCAGCGCGAGTCTTCGCACGACAGCTCGCTCGCGCTCTTC-----GAG 651
Qy 446 LysProLeuVal-----TrpLeuPheValLysPheValSerLeuValLeuPheAsnLysAla 464
Db 652 GTCCCGGTCATCCGTTGGATCACACGCCGCAAGAGCTCCCTT----- 693
Qy 465 ValLeuTrpPheGlyGlyValProGlyLysGlnTyrAlaLeuLeLysAlaAspGly 484
Db 694 -----TTCGGCTCGGCATCCGCGCGCAGCAGTTCGCAGCACTCGCGAGC----- 738
Qy 485 IleProIleGluAsnTyrIleAlaArgThrMetAspGlyValAlaGluAsnSerHisVal 504
Db 739 CTGAGCCGGAGAAATCGTCGCGCGTGTGCGCAATCGCTGGAAAGCTGACCTGT 798
Qy 505 Arg-----LysGlnAsnTyrPheTyrTyrAsnCysLeuThrGlyLysPheLeuArg 521
Db 799 CATTTCCCTTGGCGGTAATACTACTTCGCTGCGCAGGCGCTTTGCACGCGCTACCGCGG 858
Qy 522 AspAsn-----CysProThrTyrLeuArgGluAlaAlaPheAlaThrLeuLysSer 538
Db 859 CCGACGAGGGCGAGTTCCACCTTATCTTACGCATCGCATACGAGCGATTCCGCAC 918
Qy 539 GlyValValAspAsnLeuThrValSerThrAsnPhePheMetGluGluLeu----- 555
Db 919 AAT---GGGAGCGCGTCGAGTCCACCATCGAGCTTTCAGGAGCTTCTCGCGGCAAG 975
Qy 556 LysAlaArgThrTyrThrLysValIleLeuMetAspHisValAspTyrTrpLeuAspMetPro 575
Db 976 CCCCGCGCTCAGTCGACCGCTAGTGTCTCTCGACGACAGGATGGATACCGACGAC 1035
Qy 576 ValAlaAsnGluLeuAlaGluCysLeuAlaLysGlnValAlaProGlyGlyValIle 595
Db 1036 CAGCTGAACGACCTTGACCGAGATACCCGCGCGCGCGCGCGCGCGCTCGTGATC 1095
Qy 596 TrpArgSer-----AlaSerLeuSerProPro-----TyrAlaGluLeuIleGln 610
Db 1096 TTCGCGACGCGCGCGAAGCGAGCATCTCGCGGGCGCTCTCCACCACCTCTCTCGAT 1155
Qy 611 LysAlaGlyPheAspValArgCysIleArgArgAlaThrGlnGlyTyrMetAspArgVal 630
Db 1156 CAGTGGTACTATGATGCGCAGACTTCGATGAGGCTC-----GGCGCTGAAGACCGGTG 1209
Qy 631 AsnMetTyrSerSerPheTyrMetAlaArgArgLys 642
Db 1210 CGGATCTATGCGCGCTTCCACATCTACCGGAAGAAA 1245

RESULT 14
US-10-085-959-12
; Sequence 12, Application US/10085959
; Publication No. US20030165870A1
; GENERAL INFORMATION:
; APPLICANT: Blattner, Frederick R.
; APPLICANT: Welch, Rodney A.
; APPLICANT: Burland, Valerie D.
; TITLE OF INVENTION: No. US20030165870A1el Sequence of E. Coli CFT073
; FILE REFERENCE: 960296.97648
; CURRENT APPLICATION NUMBER: US/10/085,959
; CURRENT FILING DATE: 2002-03-01
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; PRIOR APPLICATION NUMBER: 60/242,412
; PRIOR FILING DATE: 2000-10-19
; NUMBER OF SEQ ID NOS: 255
; SOFTWARE: PatentIn version 3.11
; SEQ ID NO 12
; LENGTH: 4246
; TYPE: DNA
; ORGANISM: Escherichia coli
US-10-085-959-12

Alignment Scores:
Pred. No.: 0.00109 Length: 4246
Score: 128.00 Matches: 139
Percent Similarity: 34.1% Conservative: 108
Best Local Similarity: 19.2% Mismatches: 207
Query Match: 3.7% Indels: 272
DB: 6 Gaps: 40

US-10-620-914-45 (1-648) x US-10-085-959-12 (1-4246)
Qy 24 LeuSerSerMetLysAspAspLeuThrValLeuArgHisMetTrp-PheGlySerLysLy 43
Db 2393 ATTCAACACAGGCTAGGGAGGATATCCGTATCTCGCCCAACTGCAGTTTCTGCAACAAAC 2452
Qy 43 sGlyAspAspHisAlaAlaArgLeuGluSerPheTyrGlyPro-----G1 58
Db 2453 CGGTGAGTCTCACTCA-----CCATCTTCTATTCCTGACGCCAGCCTGAAC 2500
Qy 58 nAlaAlaAlaPheAlaAlaArgLeuAlaGluArgSerAsnLeuIleTrp----- 74
Db 2501 AGGCTGGCTTTTCAATG---TGCACAGAAAACCCCGAGCTAGCTGGGGTTCGGGAA 2557
Qy 75 -----ValAspLeu----- 77
Db 2558 AGCTTTCAGCTTTGAGCGAGTTATTAAACCCCTTTTGTATTGTTTAAACACTTTTGGCGT 2617
Qy 78 -----GlyGlyGlyThrGlyGluAsnValas 86
Db 2618 CTGCAACTGCAAGTGTCAACAAGAAATCAAAAGGGGGTCCCAATGGGGAACGAAAAAGA 2677
Qy 86 pMetMetAlaAspTyrIleAspLeuAlaLysPheLysSerIleTyrValValAspLeuCy 106
Db 2678 GCTTAGCGCACACCCGATGGNACTG-----TAAATATC 2710
Qy 106 sHisSerLeuCysGlu-----ValAlaLysLysLysAla-LysAlaL 120
Db 2711 ACATAGTTTTTGGCCCAAAATACCGAAGAGAGAGTGTCTACAGAGAGAGAGCTAGAGCAA 2770
Qy 120 ysgly-----TrpLysAsnValGlnValValGluAlaAspA 132
Db 2771 TAGCGCATTTTGGAGAAAGCTGTGTAGTGGAAAGCGTACGGATTCTGGAAGCTGAAT 2830
Qy 132 laCysGlnPheAlaProGluGlyThrAlaThrLeuIleThrPheSerTyrSerLeuT 152
Db 2831 GCTGT-----GCAGATCATATCATATGCTTGT 2857
Qy 152 hrMetIleProProPheHisAsnValIleAspGlnAlaCysSerTyrLeuSerGlnAspG 172
Db 2858 TGGAGATCCCGCCC-----AAAATGAGCGGTATCCG 2887
Qy 172 lyLeuValGlyValAlaAspPheTyrValSerGlyLysTyrAspLeuProLeuArgGln- 191
Db 2888 GGTTTATGGGA-----TATCTGAAGGGAAAGCAGTCTGTATGCTTTTACGAGC 2935
Qy 192 -----MetProTrpSerArgArgPhePheTrpArgSerIlePheAspI 206
Db 2936 AGTTTGGTGTGATTGAAATTCAATATACAGGAACAGGGAGTTCGTGTGACAGGGTACTACG 2995
Qy 206 leAspAsnIleAspIleGlyProGluArgArgAlaTyrLeuGluGlnLysLeuGluArgV 226
Db 2996 TCGATACAGTGGT-----NAGAACACGCGCGAAGATACAGGATTACATTAAGCACC 3046
Qy 226 alTrpGluGlnAsnThrGlnGlySerIleProTyrValProTyrValProTyrLeuArgAlaProTyr-
```


Db 1592 CCCAATAAGCAGCAGGAGTTCAACAAGCTGACAGATGATGGCCACGTGCTAGATGCT 1651
Qy 178 AspPheTyrValSerGly-----LysTyrAspLeu 187
Db 1652 GAGACCTACGTGGGGGCCACGCTGGAGGCACTAGAGTCTGGTGTCTTCAGAAGTGTATC 1711
Qy 188 Pro-----LeuArgGlnMetProTrpSerArgPhePheTrpArgSerIlePheAsp 205
Db 1712 CCCTGCCGTTAGGATGAATCCTCGACGCTTGTATTCCTGCTGCAACGAGTCGAGAG 1771
Qy 206 IleAspAsnIleAspIleGlyProGluArgAlaTyrLeuGluGln-----LysLeu 223
Db 1772 ACTATGCCCGCCGCGCATTTGAAGAAGACAGAGGTGCGCTGGAAACAGCCACCACTTT 1831
Qy 224 GluArgValTrpGluGln-----AsnThrGlnGlySerIleProTyrValPro---Trp 240
Db 1832 CAAGAGGTGTGTGAGCAGATTAAAGACCAAGCTCACCTCCCTAAAGATGTTTCTTAACAGA 1891
Qy 241 LeuArgAlaPro-----TyrTyrValTrpIleGlyArgLeu---ProSerVal----- 255
Db 1892 ATTGAATGCTCCTAATCTATCATCTAGATGTGGGGCCATGTATCTTAACATAATTCCT 1951
Qy 256 --GlyHisAlaLeuHisGluGluArgValGlu-ArgProProMetPheProProThrPh 274
Db 1952 ACCAACCCCTACAGCCTTTCGCCATAGTGTGATGAGGCCACCTGTGCTGCTGTGACTTC 2011
Qy 274 eLeuTyrThrGlnSer-----TrpGluAspProGluProAspMetGluVa 289
Db 2012 AATAAGCCTGGAGCAAGTTGTGAGAGGAAGATGGCTGGC----- 2051
Qy 289 lMetGluLeuAsnProLysAspThrValLeuThrLeuThrSerGlyGlyCysAsnAlaLe 309
Db 2052 -----AGTGGAGGGGAGAAATTC----- 2069
Qy 309 uAsnLeuLeuValGlnGlyAlaGlyGlnValValSerValAspCysAsnProAlaGlnSe 329
Db 2070 -----TGCCAGCCAGT-CGCAG 2085
Qy 329 rAlaLeuLeuGluLeuTysLysValAlaIleGlnLeuGluPheGluAspValTrpGl 349
Db 2086 TGAATACCATCGGATTTCAG-----CATCAGCTGGAGTCGGAGAGTTTCCCCC 2133
Qy 349 nLeuPheGlyGluGlyValHisProArgIleGluGluLeu----- 362
Db 2134 TTTGTTTTCAGAGGGCCAGCAGCGGCTTTTCCAGAGCTGTCCCGTGAAGAAGACGGCTAA 2193
Qy 363 -TyrGluLys--LysLeuAlaProPhe----- 370
Db 2194 ATATGAGAAGAGGAGCTGGCAGATTATTGCCGGAAGCCCTATAGAAAGATCCATGTGAC 2253
Qy 371 -----LeuSerGlnThrSerHisAsnPheTrpSerLysAr 382
Db 2254 CAAGGTAGAAGACGCTCTAATCACTACCATCTGCCAGGGGAAACTCATTTTATGTGGACAC 2313
Qy 382 gLeuTrpTyrPheGlnHisGlyLeuTyrGlnGlyMetGlyLysLeuCysTrpVa 402
Db 2314 AGTGGGGCTTCAGACAGCGCGCTATGAGTTCAAAGGACTGCACAAAGGTGTGGAAGAA 2373
Qy 402 lLeuGlnCysLeuAlaValValLeuGlyLeuGlyIlyThrValLysArgLeuAlaAsnAl 422
Db 2374 GAAGCTCTCGGAGCTGTAGAGGTGGGGGATGCATTCAGAGGTGAAGCGCTGCAAGAAC-- 2431
Qy 422 aProThrMetGluGluGlnArgArgLeuTrpAspSerAsnMetLeuIleHis----- 439
Db 2432 -----ATGGAGATCTTTTACGATTCAGTCTGAGCTGGCTCACAGTGCAT 2475
Qy 440 -----PheValLysAsnGlyProLysProLeuValTrpLeuPh 452
Db 2476 CCTGAACTCTTACGGCTATGTCATCGCAAGAGGAGCTCGC-----TGGTATTC 2526
Qy 452 eValLysPheValSerLeuValLeuPheAsnLysAlaValLeuTrpPheGlyGlyVa 472
Db 2527 CATGGAGATGGCTGGTATCTGCTGCTTTACA-----GGAGCCAAACAT 2568

Qy 472 lProGlyLysGlnTyrAlaLeuIleLysAlaAspGlyIleProfile----- 487
Db 2569 CATCACCCCAAGACAGAACTGATTGAGCAGATCGGAGGCTTTAGAAATTTGGACACCGA 2628
Qy 488 -----GluAsnTyrIleAlaArgThrMetAs 496
Db 2629 CGGAATATGGTGCTCTACCCCAATAGCTTTCCTGAAATTTTGTTCATCAAGACA----- 2683
Qy 496 pGlyValAlaGluAsnSerHisValArgLysGlnAsnTyrPheTyrTyrAsnCysLeuTh 516
Db 2684 -----ACCAATGCGAAGAACCAAACTACCATCTCTCTATCTCTGCTGCTGCTT 2733
Qy 516 rGlyLysPheLeuArgAspAsnCysProThrTyr-----LeuArgGluAlaAl 532
Db 2734 GAACATCATGTCTCAAGGAAGGCTTTTCAACACCAAGTACCAGGAACCTAACAGAGCCTTC 2793
Qy 532 aPheAlaThrLeuLysSerGlyValValAspAsnLeuThrValSerThrAsnPhePheMe 552
Db 2794 GTCTCTCACCTAT-----GTCAACCCACTCTGAGAATAGTATCTT 2832
Qy 552 tGluGluLeuLysAlaArgThrTyrThrLysValIleLeuMetAspHisValAspTrpLe 572
Db 2833 TTTTGAAGTCGATGGA---CCATACCTTGCTATGATCCTT----- 2869
Qy 572 uAspMetProValAlaAsnGluLeuAlaGluCysLeuAlaLysGlnValAlaProGlyGl 592
Db 2870 -----CCAGCCTCCCAAGGAAGCAAGAGCTGAAGAAAAGATATGCT----- 2914
Qy 592 yIleValIleTrpArgSerAlaSerLeuSerProProTyrAlaGluLeuIleGlnLysAl 612
Db 2915 ----GTGTTCAATGAAGATGTTCTCTTG-----GCTGAACCTG-----AA 2949
Qy 612 aGlyPheAspValArgCysIleArgArgAlaThrGlnGlyTyrMetAspArgValAsnMe 632
Db 2950 AGGTTTTTGAGGTGAAA-----CGCCGAGGGGAGTTGCAGCTGATTAAAAAT 2994
Qy 632 tTyr---SerSerPheTyrMetAlaArgArgLysGlyAla 644
Db 2995 ATCCAGTCTCTCAGTGTGAGGCTTCTCTCAAGGGCAGC 3034

Search completed: May 4, 2006, 18:08:56

Job time : 1427 secs

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GenCore version 5.1.7
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OM protein - nucleic search, using frame_plus_p2n model

Run on: May 4, 2006, 17:45:30 ; Search time 2237 Seconds
(without alignments)
1179.707 Million cell updates/sec

Title: US-10-620-914-45
Perfect score: 3463
Sequence: 1 MGSGRGPASTYTKNFSLE.....RVNMYSSFYMARRKGAKKDN 648

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 9306428 seqs, 2036268586 residues

Total number of hits satisfying chosen parameters: 18612856

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+ p2n.model -DEV=xlh
-Q=/abs/ABSSWEB spool/US10620914/runat 04052006 130319 18939/app query.fasta.1
-DB=Published Applications NA New -QFMT=fastap -SUFFIX=p2n.rnpbn -MINMATCH=0.1
-LOOPCL=0 -LOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum2
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100
-MAXLEN=2000000000 -HGST=abs02h
-USER=US10620914 @CGN 1.1 660 @runat 04052006 130319 18939 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOC=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications NA New:
1: /SID55/ptodata/2/pubpna/US08 NEW PUB.seq1.*
2: /SID55/ptodata/2/pubpna/US06 NEW PUB.seq.*
3: /SID55/ptodata/2/pubpna/US07 NEW PUB.seq.*
4: /SID55/ptodata/2/pubpna/US08 NEW PUB.seq.*
5: /SID55/ptodata/2/pubpna/ECT NEW PUB.seq.*
6: /SID55/ptodata/2/pubpna/US09 NEW PUB.seq.*
7: /SID55/ptodata/2/pubpna/US09 NEW PUB.seq1.*
8: /SID55/ptodata/2/pubpna/US09 NEW PUB.seq2.*
9: /SID55/ptodata/2/pubpna/US10 NEW PUB.seq.*
10: /SID55/ptodata/2/pubpna/US10 NEW PUB.seq1.*
11: /SID55/ptodata/2/pubpna/US10 NEW PUB.seq2.*
12: /SID55/ptodata/2/pubpna/US10 NEW PUB.seq3.*
13: /SID55/ptodata/2/pubpna/US10 NEW PUB.seq4.*
14: /SID55/ptodata/2/pubpna/US11 NEW PUB.seq.*
15: /SID55/ptodata/2/pubpna/US11 NEW PUB.seq2.*
16: /SID55/ptodata/2/pubpna/US11 NEW PUB.seq3.*
17: /SID55/ptodata/2/pubpna/US11 NEW PUB.seq4.*
18: /SID55/ptodata/2/pubpna/US11 NEW PUB.seq5.*
19: /SID55/ptodata/2/pubpna/US60 NEW PUB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result Query

No.	Score	Match	Length	DB	ID	Description
1	118.5	3.4	1155	17	US-11-234-786-373	Sequence 373, App
2	118.5	3.4	1155	18	US-11-139-041-301	Sequence 301, App
3	118.5	3.4	1185	18	US-11-139-041-335	Sequence 335, App
4	118.5	3.4	1590	18	US-11-139-041-323	Sequence 323, App
5	118.5	3.4	2000	17	US-11-234-786-374	Sequence 374, App
6	118.5	3.4	2000	18	US-11-139-041-302	Sequence 302, App
7	118.5	3.4	2040	17	US-11-234-786-375	Sequence 375, App
8	118.5	3.4	2040	18	US-11-139-041-303	Sequence 303, App
9	115.5	3.3	1155	18	US-11-139-041-328	Sequence 328, App
10	115.5	3.3	1512	17	US-11-234-786-368	Sequence 368, App
11	115.5	3.3	1512	18	US-11-139-041-294	Sequence 294, App
12	110	3.2	939	18	US-11-139-041-344	Sequence 344, App
13	109.5	3.2	1853	17	US-11-234-786-369	Sequence 369, App
14	109.5	3.2	1853	18	US-11-139-041-295	Sequence 295, App
15	107.5	3.1	876	18	US-11-139-041-341	Sequence 341, App
16	107.5	3.1	876	18	US-11-139-041-342	Sequence 342, App
17	107.5	3.1	879	17	US-11-234-786-531	Sequence 531, App
18	107.5	3.1	879	18	US-11-139-041-314	Sequence 314, App
19	107.5	3.1	933	18	US-11-139-041-343	Sequence 343, App
20	107.5	3.1	1852	17	US-11-234-786-530	Sequence 530, App
21	107.5	3.1	1852	18	US-11-139-041-313	Sequence 313, App
22	106	3.1	2055	18	US-11-079-463-2274	Sequence 2274, Ap
23	104	3.0	3006	11	US-10-932-182A-4215	Sequence 4215, Ap
24	104	3.0	3006	11	US-10-932-182A-4215	Sequence 4215, Ap
25	102	2.9	1857	11	US-10-932-182A-2428	Sequence 2428, Ap
26	102	2.9	1857	11	US-10-932-182A-2428	Sequence 2428, Ap
27	102	2.9	3042	17	US-11-124-367A-21	Sequence 21, Appl
28	101.5	2.9	2598	18	US-11-079-463-4664	Sequence 4664, Ap
29	101.5	2.9	7437	11	US-10-932-182A-1448	Sequence 1448, Ap
30	101.5	2.9	2067	18	US-11-079-463-2719	Sequence 2719, Ap
31	101	2.9	3063	17	US-11-169-041-29	Sequence 29, Appl
32	101	2.9	2530	10	US-10-821-234-276	Sequence 276, App
33	99.5	2.9	2229	18	US-11-072-512-652	Sequence 652, App
34	99	2.9	1457619	17	US-11-098-686-8739	Sequence 8739, Ap
35	99	2.9	2229	18	US-10-330-773-222	Sequence 222, App
36	98	2.8	26214	11	US-11-072-512-1818	Sequence 1818, Ap
37	97.5	2.8	2315	18	US-11-301-554-1894	Sequence 1894, Ap
38	97	2.8	6942	14	US-11-224-663-191	Sequence 191, App
39	97	2.8	14279	18	US-11-224-525-191	Sequence 191, App
40	97	2.8	14279	18	US-11-224-525-191	Sequence 191, App
41	97	2.8	163162	17	US-11-121-086-66	Sequence 66, Appl
42	96.5	2.8	1851	17	US-11-234-786-366	Sequence 366, App
43	96.5	2.8	1851	18	US-11-139-041-291	Sequence 291, App
44	96.5	2.8	1851	18	US-11-139-041-292	Sequence 292, App
45	96.5	2.8	2184	17	US-11-234-786-370	Sequence 370, App

ALIGNMENTS

RESULT 1
US-11-234-786-373
; Sequence 373, Application US/11234786
; Publication No. US20060024301A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Reed, Steven G.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.
; TITLE OF INVENTION: PROSTATE-SPECIFIC POLYPEPTIDES AND FUSION


```
QY 187 LeuProLeuArgGlnMetProTrrp-----SerArgArgPhePheTrpArgSerIlePhe 204
Db 204 CTTCCCTCGTCGACGGGGAGTGGCAAGACAGCAACGTGGCGCTTCTGGAGA-----254
QY 205 AspileAspAsnIleAspileGlyProGluArgArgAlaTyrLeuGluGlnLysLeuGlu 224
Db 255 -----CCACGACGACTCTGCTAT-----GAA 275
QY 225 ArgValTrpGluGlnAsnThrGlnGlySerIleProTyrValProTrrpLeuArgAlaPro 244
Db 276 GACACTCAGGAACAAGATGGGCAAGTGGTGTGCTCCACTGCTCCCTGTCGAGGGGAG 335
QY 245 TyrTyrValTrpIleGlyArgLeuProSerValGly---HisAlaLeuHisGluGluArg 263
Db 336 CGGCAAGACCAAGGTGGCGCTTGGGAGACTACGACAGTGCCTTTCATGGAGCCGAG 395
QY 264 ValGluArgProProMetPheProThrPheLeuTyrThrGlnSerTrp-GluAsp-- 282
Db 396 GTACCAAGTCCG-----TGGAGAGATCT 419
QY 283 -----ProGluProAspMetGluValMe 290
Db 420 GGACAAGCTCCACAGAGCTGCTGGTGGGTAAAGTCCCCAGAAAGGATCTCATCGTCAT 479
QY 290 t-----GluIleAsnProLysAsp-----ThrValLeuThrLeuTh 302
Db 480 GCTCAGGACACTGACGTGAACAAGAGGACAAAGAGGAGGACTGCTCTACATCTGGC 539
QY 302 rSer-----GlyGlyCysAsnAlaLeuAsnLeuValGlnGlyAlaGlyGlnValVa 320
Db 540 CTCTGCCAATGGGAATTCAGAAAGTAGTAAAGTCTCTGTCGACAGACAGTGTCAACTTAA 599
QY 320 lSerValAspCysAsnProAlaGlnSerAlaLeuLeuLysLysValAlaIleGl 340
Db 600 TGCTCTTGCAC---AACAACAAAGAGGACAGCTCTGATAAG-----GCCGTACA 644
QY 340 nGlnLeuGluPheGluAspValTrpGlnLeuPheGlyGluGlyValHisProArgIleGl 360
Db 645 ATGCCAGGAAGATGAATGTGGTTAATGTTGCTGGAAACATGGCAGCTGATCCAAATATTC 704
QY 360 uGluLeuTyr-GluLysLysLeuAlaProPheLeuSerGlnThrSerHisenPheTrps 380
Db 705 AGATGAGTATGGAATAACCATCTGCACACTGCTATCTATTAATGAAGATAAATTAATGGC 764

RESULT 3
US-11-139-041-335
; Sequence 335, Application US/11139041
; Publication No. US20060083749A1
; GENERAL INFORMATION:
; APPLICANT: Fanger, Gary R.
; APPLICANT: Hirst, Shannon Kathleen
; APPLICANT: Dillon, David C.
; APPLICANT: Foy, Teresa M.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Persing, David H.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 210121.419C15
; CURRENT APPLICATION NUMBER: US/11/139,041
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 10/079,137
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 09/924,400
; PRIOR FILING DATE: 2001-08-07
; PRIOR APPLICATION NUMBER: US 09/810,936
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: US 09/699,295
; PRIOR FILING DATE: 2000-10-26
; PRIOR APPLICATION NUMBER: US 09/590,583
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; PRIOR FILING DATE: 2000-06-08
; PRIOR APPLICATION NUMBER: US 09/577,505
; PRIOR FILING DATE: 2000-05-24
; PRIOR APPLICATION NUMBER: US 09/534,825
; PRIOR FILING DATE: 2000-03-23
; PRIOR APPLICATION NUMBER: US 09/429,755
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: US 09/289,198
; PRIOR FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: US 09/062,451
; PRIOR FILING DATE: 1998-04-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 428
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 335
; LENGTH: 1185
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-139-041-335

Alignment Scores:
Pred. No.: 0.138 Length: 1185
Score: 118.50 Matches: 66
Percent Similarity: 37.4% Conservative: 19
Best Local Similarity: 29.1% Mismatches: 81
Query Match: 3.4% Indels: 61
DB: 18 Gaps: 11

US-10-620-914-45 (1-648) x US-11-139-041-335 (1-1185)
QY 187 LeuProLeuArgGlnMetProTrrp-----SerArgArgPhePheTrpArgSerIlePhe 204
Db 204 CTTCCCTCGTCGACGGGGAGTGGCAAGACAGCAACGTGGCGCTTCTGGAGA-----254
QY 205 AspileAspAsnIleAspileGlyProGluArgArgAlaTyrLeuGluGlnLysLeuGlu 224
Db 255 -----CCACGACGACTCTGCTAT-----GAA 275
QY 225 ArgValTrpGluGlnAsnThrGlnGlySerIleProTyrValProTrrpLeuArgAlaPro 244
Db 276 GACACTCAGGAACAAGATGGGCAAGTGGTGTGCTCCACTGCTCCCTGTCGAGGGGAG 335
QY 245 TyrTyrValTrpIleGlyArgLeuProSerValGly---HisAlaLeuHisGluGluArg 263
Db 336 CGGCAAGACCAAGGTGGCGCTTGGGAGACTACGACAGTGCCTTTCATGGAGCCGAG 395
QY 264 ValGluArgProProMetPheProThrPheLeuTyrThrGlnSerTrp-GluAsp-- 282
Db 396 GTACCAAGTCCG-----TGGAGAGATCT 419
QY 283 -----ProGluProAspMetGluValMe 290
Db 420 GGACAAGCTCCACAGAGCTGCTGGTGGGTAAAGTCCCCAGAAAGGATCTCATCGTCAT 479
QY 290 t-----GluIleAsnProLysAsp-----ThrValLeuThrLeuTh 302
Db 480 GCTCAGGACACTGACGTGAACAAGAGGACAAAGAGGAGGACTGCTCTACATCTGGC 539
QY 302 rSer-----GlyGlyCysAsnAlaLeuAsnLeuValGlnGlyAlaGlyGlnValVa 320
Db 540 CTCTGCCAATGGGAATTCAGAAAGTAGTAAAGTCTCTGTCGACAGACAGTGTCAACTTAA 599
QY 320 lSerValAspCysAsnProAlaGlnSerAlaLeuLeuLysLysValAlaIleGl 340
Db 600 TGCTCTTGCAC---AACAACAAAGAGGACAGCTCTGATAAG-----GCCGTACA 644
QY 340 nGlnLeuGluPheGluAspValTrpGlnLeuPheGlyGluGlyValHisProArgIleGl 360
Db 645 ATGCCAGGAAGATGAATGTGGTTAATGTTGCTGGAAACATGGCAGCTGATCCAAATATTC 704
QY 360 uGluLeuTyr-GluLysLysLeuAlaProPheLeuSerGlnThrSerHisenPheTrps 380
Db 705 AGATGAGTATGGAATAACCATCTGCACACTGCTATCTATTAATGAAGATAAATTAATGGC 764
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Qy 380 erLysArgLeuTrpTyr 385
Db 765 CAAGACGCTGCTCTTAT 781

RESULT 4
US-11-139-041-323
; Sequence 323, Application US/111139041
; Publication No. US20060083749A1
; GENERAL INFORMATION:
; APPLICANT: Fanger, Gary R.
; APPLICANT: Hilst, Shannon Kathleen
; APPLICANT: Dillon, Davin C.
; APPLICANT: Foy, Teresa M.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Persing, David H.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 210121.419C15
; CURRENT APPLICATION NUMBER: US/11/139,041
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 10/079,137
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 09/924,400
; PRIOR FILING DATE: 2001-08-07
; PRIOR APPLICATION NUMBER: US 09/810,936
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: US 09/699,295
; PRIOR FILING DATE: 2000-10-26
; PRIOR APPLICATION NUMBER: US 09/590,583
; PRIOR FILING DATE: 2000-06-08
; PRIOR APPLICATION NUMBER: US 09/577,505
; PRIOR FILING DATE: 2000-05-24
; PRIOR APPLICATION NUMBER: US 09/534,825
; PRIOR FILING DATE: 2000-03-23
; PRIOR APPLICATION NUMBER: US 09/429,755
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: US 09/289,198
; PRIOR FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: US 09/062,451
; PRIOR FILING DATE: 1998-04-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 428
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 323
; LENGTH: 1590
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-139-041-323

Alignment Scores:
Pred. No.: 0.199 Length: 1590
Score: 118.50 Matches: 66
Percent Similarity: 37.4% Conservative: 19
Best Local Similarity: 29.1% Mismatches: 81
Query Match: 3.4% Indels: 61
DB: 18 Gaps: 11

US-10-620-914-45 (1-648) x US-11-139-041-323 (1-1590)

Qy 187 LeuProLeuArgGlnMetProTrp-----SerArgPhePheTrpArgSerIlePhe 204
Db 639 CTTCCCTGCTGCAGGGGGAGTGGCAAGACGCTGGCGCTTCTGGAGA----- 689
Qy 205 AspileAspAsnIleAspileGlyProGluArgAlaTyrLeuGluGlnLysLeuGlu 224
Db 690 -----CCACGACGACTCTCTAT-----GAA 710
Qy 225 ArgValTrpGluGlnAsnThrGlnGlySerIleProTyrValProTrpLeuArgAlaPro 244
Db 711 GACACTCAGGAACAAGATGGCAAGTGGTGGCTGTCACGTCTCCCTCTCGCAGGGGAG 770
Qy 245 TyrTyrValTrpIleGlyArgLeuProSerValGly---HisAlaLeuHisGluArg 263

```

771 CGCAAGGCAAGCTGGGCGCTTGGGAGACTACGATGACAGYGCCTTCATGGAGCCAG 830

264 ValGluArgProProMetPheProThrPheLeuTyrThrGlnSerTrp-GluAsp-- 282

831 GTACCAGTTCG-----TGGAGAAGATCT 854

283 -----ProGluProAspMetGluValMe 290

855 GGACAAGCTCCACAGAGCTGCTGGTGGGTAAAGTCCCAGAAAGGATCTCATCGTCAT 914

290 t-----GluIleAsnProLysAsp-----ThrValLeuThrLeuTh 302

915 GCTCAGGGACACTGACGTGAACAAGAGGACACAAAGAGGACTGCTCTACATCTGC 974

302 rSer-----GlyGlyCysAsnAlaLeuAsnLeuValGlnGlyAlaGlyGlnValva 320

975 CTCGTCCAATGGGAATTGAGAAGTAGTAAAACTCTGCTGGACACAGCATGTCAACTTAA 1034

320 lSerValAspCysAsnProAlaGlnSerAlaLeuLeuGluLeuLysLysValAlaIleGl 340

1035 TGTCTTGTAC---AACAAAAGAGGACAGCTCTGTATAAG-----GCCGTACA 1079

340 nGlnLeuGluPheGluAspValTrpGlnLeuPheGlyGlyValHisProArgIleGl 360

1080 ATGCCAGGAAGATGAATGCGTTAATGTTGCTGGAACATGCGCACTGATCCAAATATTC 1139

360 uGluLeuTyr-GluLysLysLeuAlaProPheLeuSerGlnThrSerHisAsnHeTrpS 380

1140 AGATGAGTATGGAATACCACTCTGCACTAGCTATCTATTAATGAAGATAAATTAATGCG 1199

380 erLysArgLeuTrpTyr 385

1200 CAAGACGCTGCTCTTAT 1216

RESULT 5

US-11-234-786-374

; Sequence 374, Application US/11234786

; Publication No. US20060024301A1

; GENERAL INFORMATION:

; APPLICANT: Xu, Jiangchun

; APPLICANT: Dillon, Davin C.

; APPLICANT: Mitcham, Jennifer L.

; APPLICANT: Harlocker, Susan L.

; APPLICANT: Jiang, Yuqiu

; APPLICANT: Reed, Steven G.

; APPLICANT: Kalos, Michael D.

; APPLICANT: Fanger, Gary R.

; APPLICANT: Retter, Marc W.

; APPLICANT: Stolk, John A.

; APPLICANT: Day, Craig H.

; APPLICANT: Vedvick, Thomas S.

; APPLICANT: Carter, Darrick

; APPLICANT: Li, Samuel X.

; APPLICANT: Wang, Aijun

; APPLICANT: Skeiky, Yasir A.

; TITLE OF INVENTION: PROSTATE-SPECIFIC POLYPEPTIDES AND FUSION

; TITLE OF INVENTION: POLYPEPTIDES THEREOF

; FILE REFERENCE: 210121.427C31

; CURRENT APPLICATION NUMBER: US/11/234,786

; CURRENT FILING DATE: 2005-09-23

; PRIOR APPLICATION NUMBER: US 09/568,857

; PRIOR FILING DATE: 2000-05-09

; PRIOR APPLICATION NUMBER: US 09/536,857

; PRIOR FILING DATE: 2000-05-27

; PRIOR APPLICATION NUMBER: US 09/483,672

; PRIOR FILING DATE: 2000-01-14

; PRIOR APPLICATION NUMBER: US 09/439,313

; PRIOR FILING DATE: 1999-11-12

; PRIOR APPLICATION NUMBER: US 09/352,616

; PRIOR FILING DATE: 1999-07-13

; PRIOR APPLICATION NUMBER: US 09/288,946

; PRIOR FILING DATE: 1999-04-09

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Db      765 CAAAGCACTGCTCTAT 781

RESULT 6
US-11-139-041-302
; Sequence 302, Application US/11139041
; Publication No. US20060083749A1
; GENERAL INFORMATION: Gary R.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Hirst, Shannon Kathleen
; APPLICANT: Dillon, Davin C.
; APPLICANT: Foy, Teresa M.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Persing, David H.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; OF INVENTION: AND DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 210121.419C15
; CURRENT APPLICATION NUMBER: US/11/139,041
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 10/079,137
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 09/924,400
; PRIOR FILING DATE: 2001-08-07
; PRIOR APPLICATION NUMBER: US 09/810,936
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: US 09/699,295
; PRIOR FILING DATE: 2000-10-26
; PRIOR APPLICATION NUMBER: US 09/590,583
; PRIOR FILING DATE: 2000-06-08
; PRIOR APPLICATION NUMBER: US 09/577,505
; PRIOR FILING DATE: 2000-05-24
; PRIOR APPLICATION NUMBER: US 09/534,825
; PRIOR FILING DATE: 2000-03-23
; PRIOR APPLICATION NUMBER: US 09/429,755
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: US 09/289,198
; PRIOR FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: US 09/062,451
; PRIOR FILING DATE: 1998-04-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 428
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 302
; LENGTH: 2000
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-139-041-302

Alignment Scores:
Pred. No.: 0.265 Length: 2000
Score: 118.50 Matches: 66
Percent Similarity: 37.4% Conservative: 19
Best Local Similarity: 29.1% Mismatches: 81
Query Match: 3.4% Indels: 61
DB: 18 Gaps: 11

US-10-620-914-45 (1-648) x US-11-139-041-302 (1-2000)

Qy 187 LeuProLeuArgGlnMetProTrp-----SerArgPhePheTrpArgSerIlePhe 204
Db 204 CTTCCCTGCTGCAGGGGGAGTGCAAGAGCAAGCTGGCGCTCTCGAGA----- 254
Qy 205 AspIleAspAsnIleAspIleGlyProGluArgArgAlaTyrLeuGluGlnLysLeuGlu 224
Db 255 -----CCACGACGACTCTGCTAT-----GAA 275
Qy 225 ArgValTrpGluGlnAsnThrGlnGlySerIleProTyrValProTrpLeuArgAlaPro 244
Db 276 GACACTCAGGACCAAGATGGCGAAGTGGTGTGCACTGCTTCCCTGTCGAGGGGAG 335
Qy 245 TyrTyrValTrpIleGlyArgLeuProSerValGly---HisAlaLeuHisGluGluArg 263
Db 336 CGGCAAGAGCAAGTGGTGGCGCTTGGGGAGACTACGATGACAGTGCCTTCATGGACCCAG 395

```


US-11-139-041-303
; Sequence 303, Application US/11139041
; Publication No. US20060083749A1
; GENERAL INFORMATION:
; APPLICANT: Panger, Gary R.
; APPLICANT: Hirst, Shannon Kathleen
; APPLICANT: Dillon, Davin C.
; APPLICANT: Foy, Teresa M.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Persing, David H.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 210121.419C15
; CURRENT APPLICATION NUMBER: US/11/139,041
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 10/079,137
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 09/924,400
; PRIOR FILING DATE: 2001-08-07
; PRIOR APPLICATION NUMBER: US 09/810,936
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: US 09/699,295
; PRIOR FILING DATE: 2000-10-26
; PRIOR APPLICATION NUMBER: US 09/590,583
; PRIOR FILING DATE: 2000-06-08
; PRIOR APPLICATION NUMBER: US 09/577,505
; PRIOR FILING DATE: 2000-05-24
; PRIOR APPLICATION NUMBER: US 09/534,825
; PRIOR FILING DATE: 2000-03-23
; PRIOR APPLICATION NUMBER: US 09/429,755
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: US 09/289,198
; PRIOR FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: US 09/062,451
; PRIOR FILING DATE: 1998-04-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 428
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 303
; LENGTH: 2040
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-139-041-303

Alignment Scores:
Pred. No.: 0, 272 Length: 2040
Score: 118.50 Matches: 66
Percent Similarity: 37.4% Conservative: 19
Best Local Similarity: 29.1% Mismatches: 81
Query Match: 3.4% Indels: 61
DB: 18 Gaps: 11

US-10-620-914-45 (1-648) x US-11-139-041-303 (1-2040)

Qy 187 LeuProLeuArgGlnMetProTyr-----SerArgArgPhePheTyrArgSerIlePhe 204
Db 204 CTTCCTGCTGCAGGGGGAGTGGCAAGCAACGTGGCGCTCTCGAGA-----254
Qy 205 AspIleAspAsnIleAspIleProGluArgArgAlaTyrLeuGluGlnLysLeuGlu 224
Db 255 -----CCAGCAGCAGCTCTGCTAT-----GAA 275
Qy 225 ArgValTyrGluGlnAsnThrGlnGlySerIleProTyrValProTyrLeuArgAlaPro 244
Db 276 GACACTCAGGAACAAGATGGGAAGTGTGCTGCCACTGCTTCCCTGTCGAGGGGAG 335
Qy 245 TyrTyrValTyrIleGlyArgLeuProSerValGly---HisAlaLeuHisGluGluArg 263
Db 336 CGGCAAGCAAGTGGCGCTTGGGAGACTACGATGACAGTGCCTTCATGGAGCCCG 395
Qy 264 ValGluArgProProMetPheProProThrPheLeuTyrThrGlnSerTyrGluAsp-- 282
Db 396 GTACCACGTCGG-----TGGAGAAGATCT 419

Qy 283 -----ProGluProAspMetGluValMe 290
Db 420 GGCAAGCTCCACAGAGCTGCTGGTGGGTAAAGTCCCAAGAGGATCTCATCGTCAT 479
Qy 290 t-----GluLeuAsnProLysAsp-----ThrValLeuThrLeuTh 302
Db 480 GCTCAGGACACTGACGTGAACAAGAGGACCAAGCAAAAGAGGACTGCTCTACATCTGGC 539
Qy 302 rSer-----GlyGlyCysAsnAlaLeuAsnLeuValGlnGlyAlaGlyGlnValVa 320
Db 540 CTCTGCCAATGGGAATTGAGAGTAGTAAACTCTGCTGGACAGACCATGCAACTTAA 599
Qy 320 lSerValAspCysAsnProAlaGlnSerAlaLeuLeuGluLeuLysValAlaIleGl 340
Db 600 TGTCTTGAC---AACAAAAAGAGACAGCTCTGATAAG-----GCCGTACA 644
Qy 340 nGlnLeuGluPheGluAspValTyrGlnLeuPheGlyGlyGlyValHisProArgIleGl 360
Db 645 ATGCCAGGAAGATGAATGTCGTTAATGTTCTGGAAACATGGCACTGATCCAAATATTCC 704
Qy 360 uGluLeuTyr-GluLysLysLeuAlaProPheLeuSerGlnThrSerHisAsnPheTrps 380
Db 705 AGATGAGTATGGAATACCACTCTGCACCTACCTATCTATATGAGATAAATTAATGGC 764
Qy 380 erLysArgLeuTyrTyr 385
Db 765 CAAGCAGCTGCTCTTAT 781

RESULT 9
US-11-139-041-328
; Sequence 328, Application US/11139041
; Publication No. US20060083749A1
; GENERAL INFORMATION:
; APPLICANT: Panger, Gary R.
; APPLICANT: Hirst, Shannon Kathleen
; APPLICANT: Dillon, Davin C.
; APPLICANT: Foy, Teresa M.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Persing, David H.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 210121.419C15
; CURRENT APPLICATION NUMBER: US/11/139,041
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 10/079,137
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 09/924,400
; PRIOR FILING DATE: 2001-08-07
; PRIOR APPLICATION NUMBER: US 09/810,936
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: US 09/699,295
; PRIOR FILING DATE: 2000-10-26
; PRIOR APPLICATION NUMBER: US 09/590,583
; PRIOR FILING DATE: 2000-06-08
; PRIOR APPLICATION NUMBER: US 09/577,505
; PRIOR FILING DATE: 2000-05-24
; PRIOR APPLICATION NUMBER: US 09/534,825
; PRIOR FILING DATE: 2000-03-23
; PRIOR APPLICATION NUMBER: US 09/429,755
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: US 09/289,198
; PRIOR FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: US 09/062,451
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 428
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 328
; LENGTH: 1155
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-139-041-328

Db 642 GGACAAAGCTCCACAGAGCTGCTGGTAAAGTCCCAAGAGGATCTCATCGTCAT 701
QY 290 t-----GluileAsnProLysAsp-----ThrValLeuThrLeuTh 302
Db 702 GCTCAGGGACACTGACGTGAACAGAGGACAAAGAGGAGGAGGAGGAGGAGGAG 761
QY 302 rSer-----GlyGlyCysAsnAlaLeuAsnLeuValGlnGlyAlaGlyValVa 320
Db 762 CTCTCCCAATGGGAATTCAGAAAGTAGTAAACTGTGCTGGACAGACGATGCAACTTAA 821
QY 320 lSerValAspCysAsnProAlaGlnSerAlaLeuLeuGluLeuLysValAlaIleGl 340
Db 822 TGTCTCTGAC---AACAAAAGAGGACAGCTCTGAYAAAG-----GCCGTACA 866
QY 340 nGlnLeuGluPheGluAspValTrpGlnLeuPheGlyGluGlyValHisProArgIleGl 360
Db 867 ATGCCAGGAAGATGAATGCGCTTAATGTTGCTGGAACATGCGACTGATCCAAATATTCC 926
QY 360 uGluLeuTyr-GluLysLysLeuAlaProPheLeuSerGlnThrSerHisAsnPheTrpS 380
Db 927 AGATGAGTATGGAATACACTCTRCACCTAYGCTRTCTAYAAATGAAGATAAATAATGGC 986
QY 380 erLysArgLeuTrpTyr 385
Db 987 CAAGCACTGCTCTTAT 1003

RESULT 11

US-11-139-041-294
; Sequence 294, Application US/11139041
; Publication No. US20060083749A1
; GENERAL INFORMATION:
; APPLICANT: Fanger, Gary R.
; APPLICANT: Hirst, Shannon Kathleen
; APPLICANT: Dillon, Davin C.
; APPLICANT: Foy, Teresa M.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Persing, David H.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 210121.419C15
; CURRENT APPLICATION NUMBER: US/11/139,041
; PRIOR FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 10/079,137
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 09/924,400
; PRIOR FILING DATE: 2001-08-07
; PRIOR APPLICATION NUMBER: US 09/810,936
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: US 09/699,295
; PRIOR FILING DATE: 2000-10-26
; PRIOR APPLICATION NUMBER: US 09/590,583
; PRIOR FILING DATE: 2000-06-08
; PRIOR APPLICATION NUMBER: US 09/577,505
; PRIOR FILING DATE: 2000-05-24
; PRIOR APPLICATION NUMBER: US 09/534,825
; PRIOR FILING DATE: 2000-03-23
; PRIOR APPLICATION NUMBER: US 09/429,755
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: US 09/289,198
; PRIOR FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: US 09/062,451
; PRIOR FILING DATE: 1998-04-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 428
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 294
; LENGTH: 1512
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-139-041-294

Alignment Scores:

Pred. No.: 0.374 Length: 1512

Score: 115.50 Matches: 65
Percent Similarity: 36.6% Conservative: 18
Best local Similarity: 28.6% Mismatches: 83
Query Match: 3.3% Indels: 61
DB: 18 Gaps: 11

US-10-620-914-45 (1-648) x US-11-139-041-294 (1-1512)

QY 187 LeuProLeuArgGlnMetProTrp-----SerArgArgPhePheTrpArgSerIlePhe 204
Db 426 CTTCCCTGCTGCGAGGGGAGTGGCAAGAGCAACGTCGGCGCTTCTGGAGA-----476
QY 205 AspIleAspAsnIleAspIleGlyProGluArgArgAlaTyrLeuGluGlnLysLeuGlu 224
Db 477 -----CCACGACGAYTCTGCTAT-----GAA 497
QY 225 ArgValTrpGluGlnAsnThrGlnGlySerIleProTyrValProTrpLeuArgAlaPro 244
Db 498 GACACTCAGGAACAGATGGGCAAGTGGTGTGCCACTGCTTCCCTGCTGCGAGGGGAG 557
QY 245 TyrTyrValTrpIleGlyArgLeuProSerValGly---HisAlaLeuHisGluGluArg 263
Db 558 CRGCAAGAGCAAGGTGGGCGCTTGGGGAGACTACGATCACAGTGCCTTCATGGAGCCGAG 617
QY 264 ValGluArgProProMetPheProProThrPheLeuTyrThrGlnSerTrp-GluAsp-- 282
Db 618 GTACCACGTCGG-----TGGAGAAAGATCT 641
QY 283 -----ProGluProAspMetGluValMe 290
Db 642 GGACAAAGCTCCACAGAGCTGCTGGTGGGTTAAAGTCCCAAGAGGATCTCATCGTCAT 701
QY 290 t-----GluileAsnProLysAsp-----ThrValLeuThrLeuTh 302
Db 702 GCTCAGGGACACTGACGTGAACAGAGGACAAAGAGGAGGAGGAGGAGGAGGAGGAG 761
QY 302 rSer-----GlyGlyCysAsnAlaLeuAsnLeuValGlnGlyAlaGlyValVa 320
Db 762 CTCTGCCAATGGGAATTCAGAAAGTAGTAAACTCTGCTGGACAGACGATGCAACTTAA 821
QY 320 lSerValAspCysAsnProAlaGlnSerAlaLeuLeuGluLeuLysValAlaIleGl 340
Db 822 TGTCTCTGAC---AACAAAAGAGGACAGCTCTGAYAAAG-----GCCGTACA 866
QY 340 nGlnLeuGluPheGluAspValTrpGlnLeuPheGlyGlyValHisProArgIleGl 360
Db 867 ATGCCAGGAAGATGAATGCGCTTAATGTTGCTGGAACATGCGACTGATCCAAATATTCC 926
QY 360 uGluLeuTyr-GluLysLysLeuAlaProPheLeuSerGlnThrSerHisAsnPheTrpS 380
Db 927 AGATGAGTATGGAATACACTCTRCACCTAYGCTRTCTAYAAATGAAGATAAATAATGGC 986
QY 380 erLysArgLeuTrpTyr 385
Db 987 CAAGCACTGCTCTTAT 1003

RESULT 12

US-11-139-041-344
; Sequence 344, Application US/11139041
; Publication No. US20060083749A1
; GENERAL INFORMATION:
; APPLICANT: Fanger, Gary R.
; APPLICANT: Hirst, Shannon Kathleen
; APPLICANT: Dillon, Davin C.
; APPLICANT: Foy, Teresa M.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Persing, David H.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 210121.419C15
; CURRENT APPLICATION NUMBER: US/11/139,041
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 10/079,137

```
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 09/924,400
; PRIOR FILING DATE: 2001-08-07
; PRIOR APPLICATION NUMBER: US 09/810,936
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: US 09/699,295
; PRIOR FILING DATE: 2000-10-26
; PRIOR APPLICATION NUMBER: US 09/590,583
; PRIOR FILING DATE: 2000-06-08
; PRIOR APPLICATION NUMBER: US 09/577,505
; PRIOR FILING DATE: 2000-05-24
; PRIOR APPLICATION NUMBER: US 09/534,825
; PRIOR FILING DATE: 2000-03-23
; PRIOR APPLICATION NUMBER: US 09/429,755
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: US 09/289,198
; PRIOR FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: US 09/062,451
; PRIOR FILING DATE: 1998-04-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 428
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 344
; LENGTH: 939
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-139-041-344

Alignment Scores:
Pred. No.: 0, 738 Length: 939
Score: 110.00 Matches: 63
Percent Similarity: 36.3% Conservative: 22
Best Local Similarity: 26.9% Mismatches: 85
Query Match: 3.2% Indels: 64
DB: 18 Gaps: 11

US-10-620-914-45 (1-648) x US-11-139-041-344 (1-939)
Qy 183 GlyIystrAspLeuProLeuArgGlnMetProTrpSerArg- 197
Db 72 GGGCAAGTGTGCTGCCACTGCTTCCCTGCTGCGAGGGGAGCGCAAGAGCAACGTGGG 131
Qy 198 PhehetrArgSerilePheaspIleaspIleaspIleGlyProGluArgAla 217
Db 132 CACTCTCGAGA- 158
Qy 218 TyrLeuGluGlnLysLeuGluArgValTrpGluGlnAsnThrGlnGlySerIleProTyr 237
Db 159 -----TGTAAGACGCTTGGGAGCAAGAGTCCAAGTGTGCTGCCACTG 203
Qy 238 ValProTrpLeuArgAlaProTyrTyrValTrpIleGlyArgLeuProSerValGly--- 256
Db 204 CTTCCCTGCTGCAGGGGAGCGGCAAGAGCAACGTGCTTGGGGAGACTACGATGA 263
Qy 257 HisAlaLeuHisGluGluArgValGluArgProProMetPheProThrPheLeuTyr 276
Db 264 CAGCGCCCTTCATGGATCCAGGTACCCAGTCCA- 296
Qy 277 ThrGlnSerTrp-GluAsp- 283
Db 297 -----TGAGAGAGATCTGGACAAGCTCCACAGAGCTGCCTGGTGGGTAAAGTCCC 347
Qy 283 oGluProAspMetGluValMet-----GluIleAsnProLysAsp----- 296
Db 348 CAGAAAGGATCTCATCGTCTGCTCAGGAGACCGGATGTGAACAAGAGGACAGCAAAA 407
Qy 297 ----ThrValLeuThrLeuThrSer-----GlyGlyCysAsnAlaLeuAsnLeuVal 313
Db 408 GAGGACTGCTCTACATCTGGCCTCTGCCAATGGGAATTGAGAAGTAGTAAATCGTGCT 467
Qy 313 LglnGlyAlaGlyGlnValSerValAspCysAsnProAlaGlnSerAlaLeuGln 333
Db 468 GGACAGACGATGTCAACTTAATGTCTTGAC----ACAAAGAGGACGAGCTCTGACAAA 524
```

```
Qy 333 uLeuLysLysValAlaIleGlnLeuGluPheGluAspValTrpGlnLeuPheGlyG1 353
Db 525 G-----GCCGTACAATGCCAGGAAGATGTCGTTAATGTTGCTGGAACA 572
Qy 353 uGlyValHisProArgIleGluGluLeuTyr-GluLysLysLeuAlaProPheLeuSerG 373
Db 573 TGGCACTGATCCAATATTCAGATGAGTATGGAAATACCACTCTACACTATGCTGCTA 632
Qy 373 lnThrSerHisAsnPheTrpSerLysArgLeuTrpTyr 385
Db 633 CAATGAAGATAAATAATATGGCCAAAGCACTGCTCTTAT 670
```

```
RESULT 13
US-11-234-786-369
; Sequence 369, Application US/11234786
; Publication No. US20060024301A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yudi
; APPLICANT: Reed, Steven G.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedwick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.
; TITLE OF INVENTION: PROSTATE-SPECIFIC POLYPEPTIDES AND FUSION
; FILE REFERENCE: 210121.427C31
; CURRENT APPLICATION NUMBER: US/11/234,786
; PRIOR FILING DATE: 2005-09-23
; PRIOR APPLICATION NUMBER: US 09/568,857
; PRIOR FILING DATE: 2000-05-09
; PRIOR APPLICATION NUMBER: US 09/536,857
; PRIOR FILING DATE: 2000-05-27
; PRIOR APPLICATION NUMBER: US 09/483,672
; PRIOR FILING DATE: 2000-01-14
; PRIOR APPLICATION NUMBER: US 09/439,313
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: US 09/352,616
; PRIOR FILING DATE: 1999-07-13
; PRIOR APPLICATION NUMBER: US 09/288,946
; PRIOR FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: US 09/232,149
; PRIOR FILING DATE: 1999-01-15
; PRIOR APPLICATION NUMBER: US 09/159,812
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: US 09/115,453
; PRIOR FILING DATE: 1998-07-14
; PRIOR APPLICATION NUMBER: US 09/030,607
; PRIOR FILING DATE: 1998-02-25
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 701
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 369
; LENGTH: 1853
; TYPE: DNA
; ORGANISM: Homo sapien
US-11-234-786-369
```

```
Alignment Scores:
Pred. No.: 1.92 Length: 1853
Score: 109.50 Matches: 64
Percent Similarity: 36.1% Conservative: 18
Best Local Similarity: 28.2% Mismatches: 84
```


Db 867 ATGCCAGGAGATGAATGTCGCTTAATGTCGTGGAACATGCCTGATCCAAATATTC 926
Qy 360 uGluLeuTyr-GluLysLysLeuAlaProPheLeuSerGlnThrSerHisAsnPheTrpS 380
Db 927 AGATGAGTATGGAATACCACTCTRCACCTACTGCTRTCTCTAYAAATGAAGATAAAATTAATGGC 986
Qy 380 erLysArgLeuTrpTyr 385
Db 997 CAAGACACTGCTCTTAT 1003

RESULT 15

US-11-139-041-341
; Sequence 341, Application US/11139041
; Publication No. US20060083749A1
; GENERAL INFORMATION:
; APPLICANT: Fanger, Gary R.
; APPLICANT: Hirst, Shannon Kathleen
; APPLICANT: Dillon, Davin C.
; APPLICANT: Foy, Teresa M.
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Persing, David H.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; OF INVENTION: AND DIAGNOSIS OF BREAST CANCER

FILE REFERENCE: 210121.419C15
CURRENT APPLICATION NUMBER: US/11/139,041

CURRENT FILING DATE: 2005-05-25
PRIOR APPLICATION NUMBER: US 10/079,137
PRIOR FILING DATE: 2002-02-20
PRIOR APPLICATION NUMBER: US 09/924,400
PRIOR FILING DATE: 2001-08-07
PRIOR APPLICATION NUMBER: US 09/810,936
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: US 09/699,295
PRIOR FILING DATE: 2000-10-26
PRIOR APPLICATION NUMBER: US 09/590,583
PRIOR FILING DATE: 2000-06-08
PRIOR APPLICATION NUMBER: US 09/577,505
PRIOR FILING DATE: 2000-05-24
PRIOR APPLICATION NUMBER: US 09/534,825
PRIOR FILING DATE: 2000-03-23
PRIOR APPLICATION NUMBER: US 09/429,755
PRIOR FILING DATE: 1999-10-28
PRIOR APPLICATION NUMBER: US 09/289,198
PRIOR FILING DATE: 1999-04-09
PRIOR APPLICATION NUMBER: US 09/062,451
PRIOR FILING DATE: 1998-04-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 428
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 341
; LENGTH: 876
; TYPE: DNA
; ORGANISM: Homo sapiens

US-11-139-041-341

Alignment Scores:
Pred. No.: 1.2 Length: 876
Score: 107.50 Matches: 59
Percent Similarity: 36.6% Conservative: 20
Best Local Similarity: 27.3% Mismatches: 78
Query Match: 3.1% Indels: 59
DB: 18 Gaps: 10

US-10-620-914-45 (1-648) x US-11-139-041-341 (1-876)

Qy 196 ArgArgPhePheTrpArgSerIlePheAspIleAsnIleAspIleGlyProGluArg 215
Db 63 CGTGGGCACCTCTGGAGA-----CCACAACA 89
Qy 216 ArgAlaTyrLeuGluGlnLysLeuGluArgValTrpGluGlnAsnThrGlnGlySerIle 235
Db 90 CTCCTC-----TGTGAAGACGCTTGGAGACAAGAGGTGCAAGTGTGCTG 134

Qy 236 ProTyrValProTyrLeuArgAlaProTyrTyrValTrpIleGlyArgLeuProSerVal 255
Db 135 CCACCTGCTTCCCTGCTGTCAGGGAGCGGCAAGAGCAACGTGTGCTTGGGGAGACTA 194
Qy 256 Gly---HisAlaLeuHisGluGluArgValGluArgProProMetPheProThrPhe 274
Db 195 CGATGACAGCGCCTTCATGGATCCAGGTACACGTCCA----- 233
Qy 275 LeuTyrThrGlnSerTrp-GluAsp----- 282
Db 234 -----TGGAGAAGATCTGGACAAGCTCCACAGAGCTGCCTGGTGGGTAA 278
Qy 283 -----ProGluProAspMetGluValMet-----GluIleAsnProLysAsp-- 296
Db 279 AGTCCCAGAAAGGATCTCATGTCATGCTCAGGGACACGGATGTGAACAAGAGGACAA 338
Qy 297 -----ThrValLeuThrLeuThrSer-----GlyGlyCysAsnAlaLeuAsnLe 311
Db 339 GCAAAAGAGGACTGCTCTACATCTGGCTCTGCGCAATGGGAATTCAGAAAGTAGTAAACT 398
Qy 311 uLeuValGlnGlyAlaGlyGlnValSerValAspCysAsnProAlaGlnSerAlaLe 331
Db 399 CGTCTGGACAGACGATGTCAACTTAATGTCCTTGAC---AACAAAAGAGGACAGCTCT 455
Qy 331 uLeuGluLeuLysLysValAlaIleGlnGlnLeuGluPheGluAspValTrpGlnLeuPh 351
Db 456 GACAAAG-----GCCGTACAAATGCCAGGAAGATGAATGCGTTAATGTTGCT 503
Qy 351 eGlyGluGlyValHisProArgIleGluGluLeuTyr-GluLysLysLeuAlaProPheL 371
Db 504 GGAACATGGCCTGATCCAAATATTCAGATGAGTATGGAAATACCACTCTACACTATGC 563
Qy 371 euSerGlnThrSerHisAsnPheTrpSerLysArgLeuTrpTyr 385
Db 564 TGTCTACAATGAAGATAAATTAATGGCCAAAGCACTGCTCTTAT 607

Search completed: May 4, 2006, 18:45:27
Job time : 2251 secs